

FIG. 1A

FIG. 1B

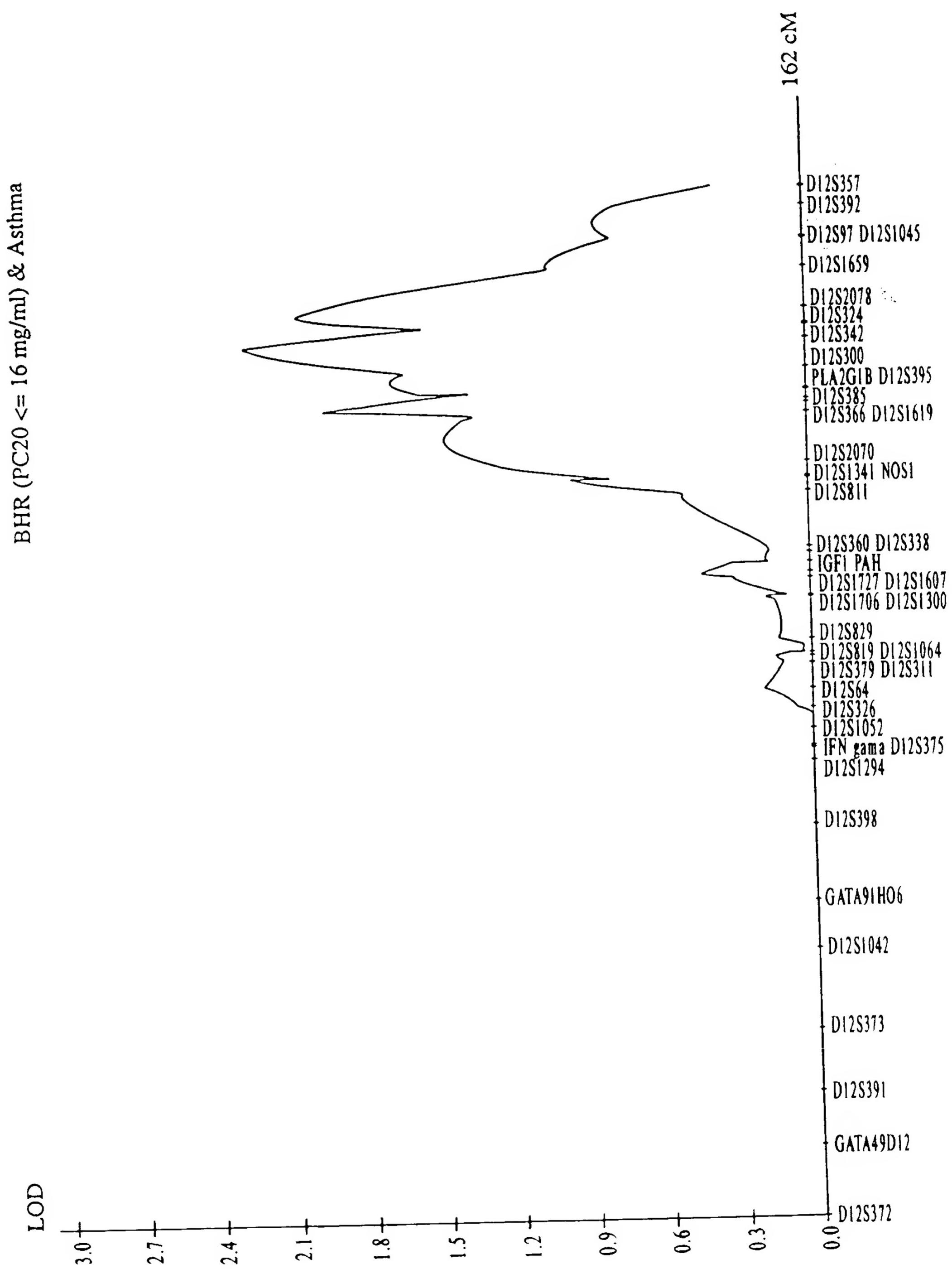


FIG. 1C

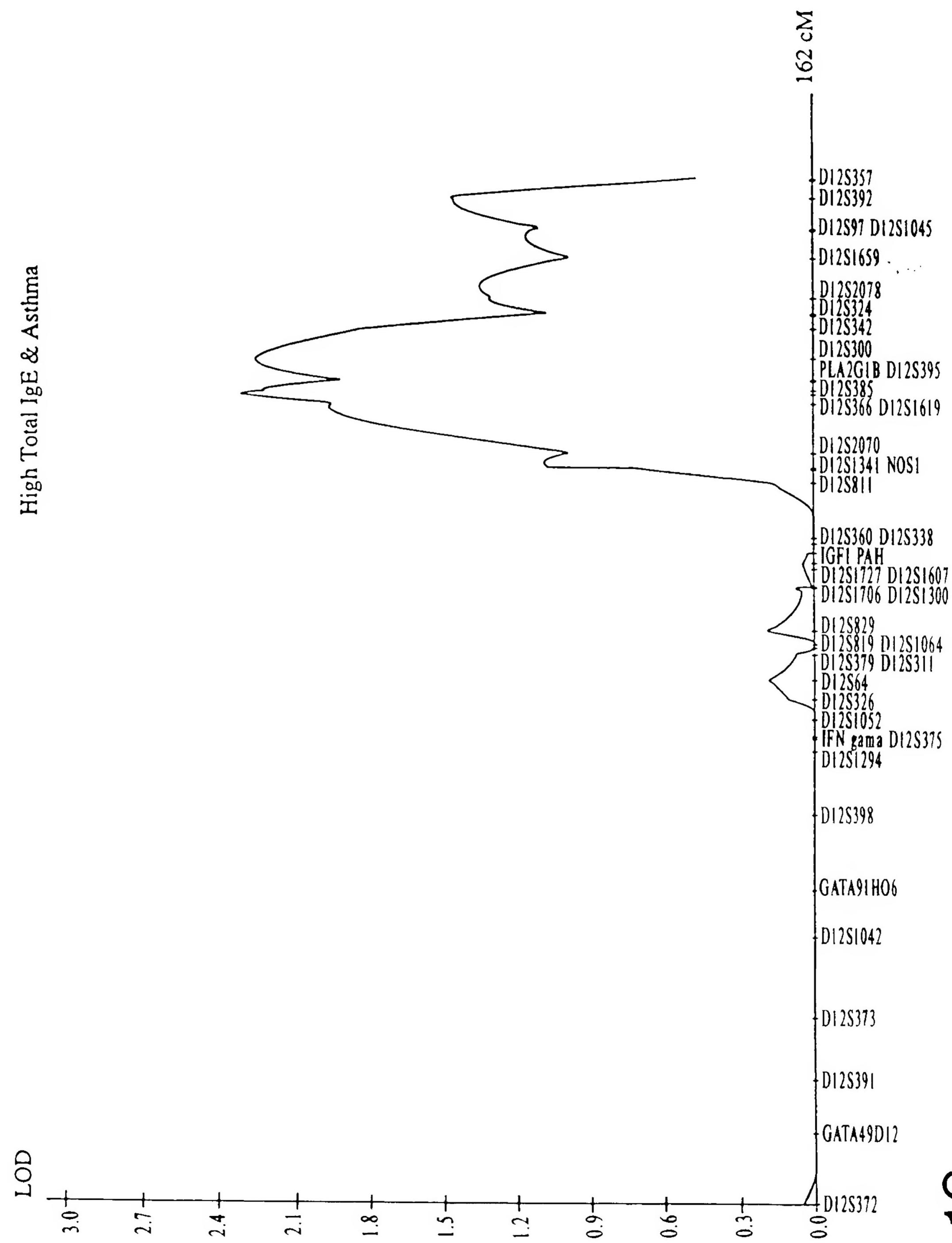
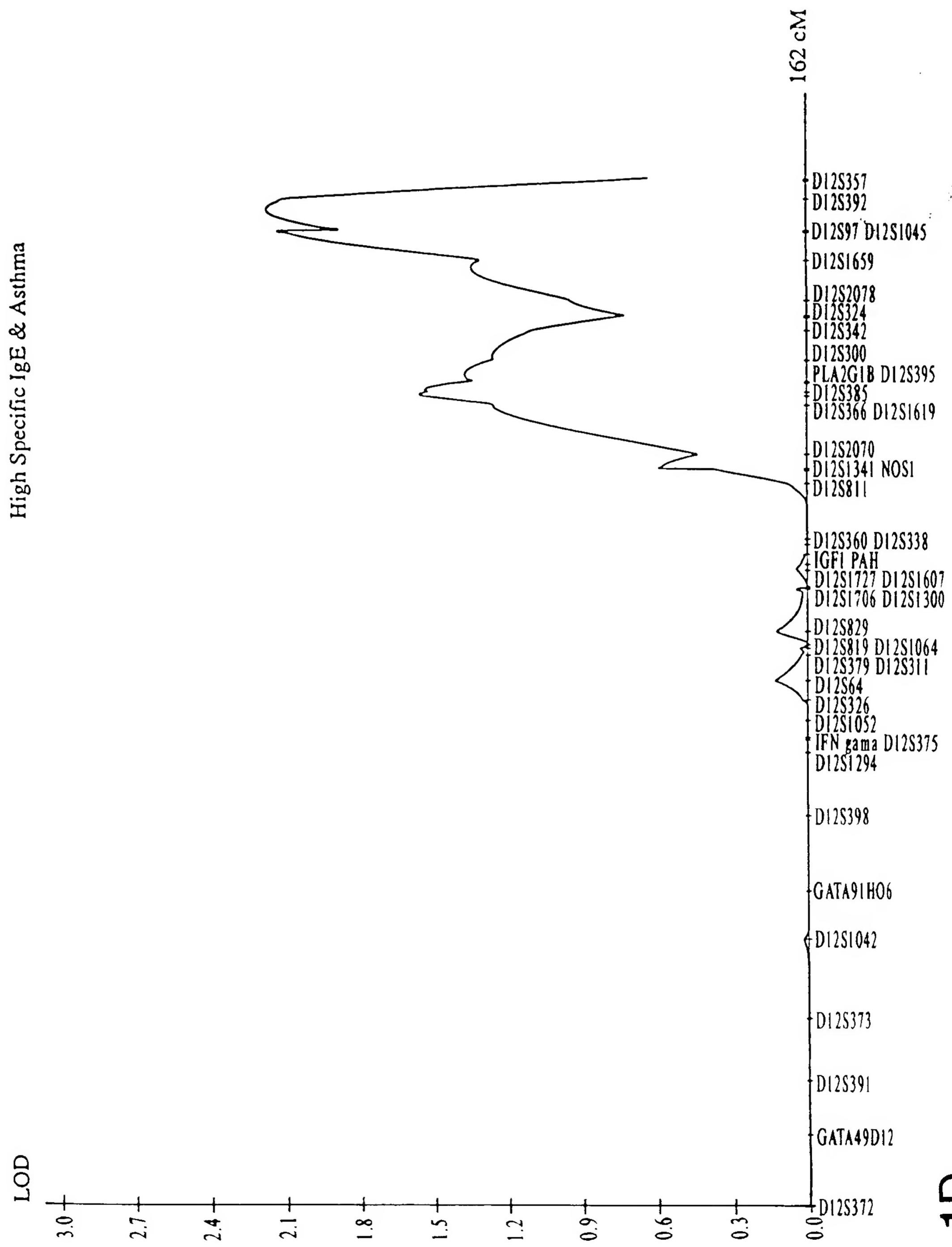
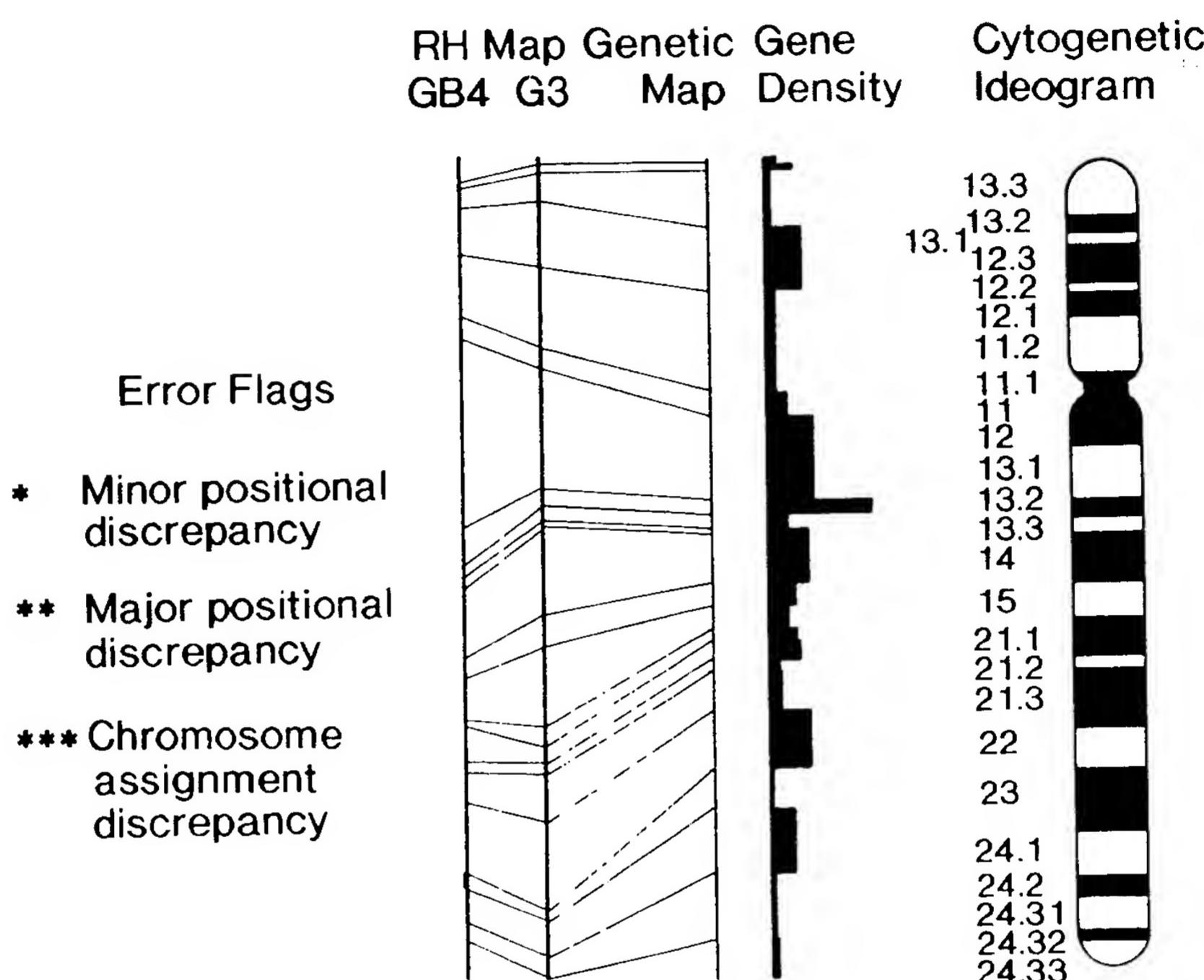


FIG. 1D



Chromosome 12: D12S79-D12S366



- Error Flags**
- * Minor positional discrepancy
 - ** Major positional discrepancy
 - *** Chromosome assignment discrepancy

The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

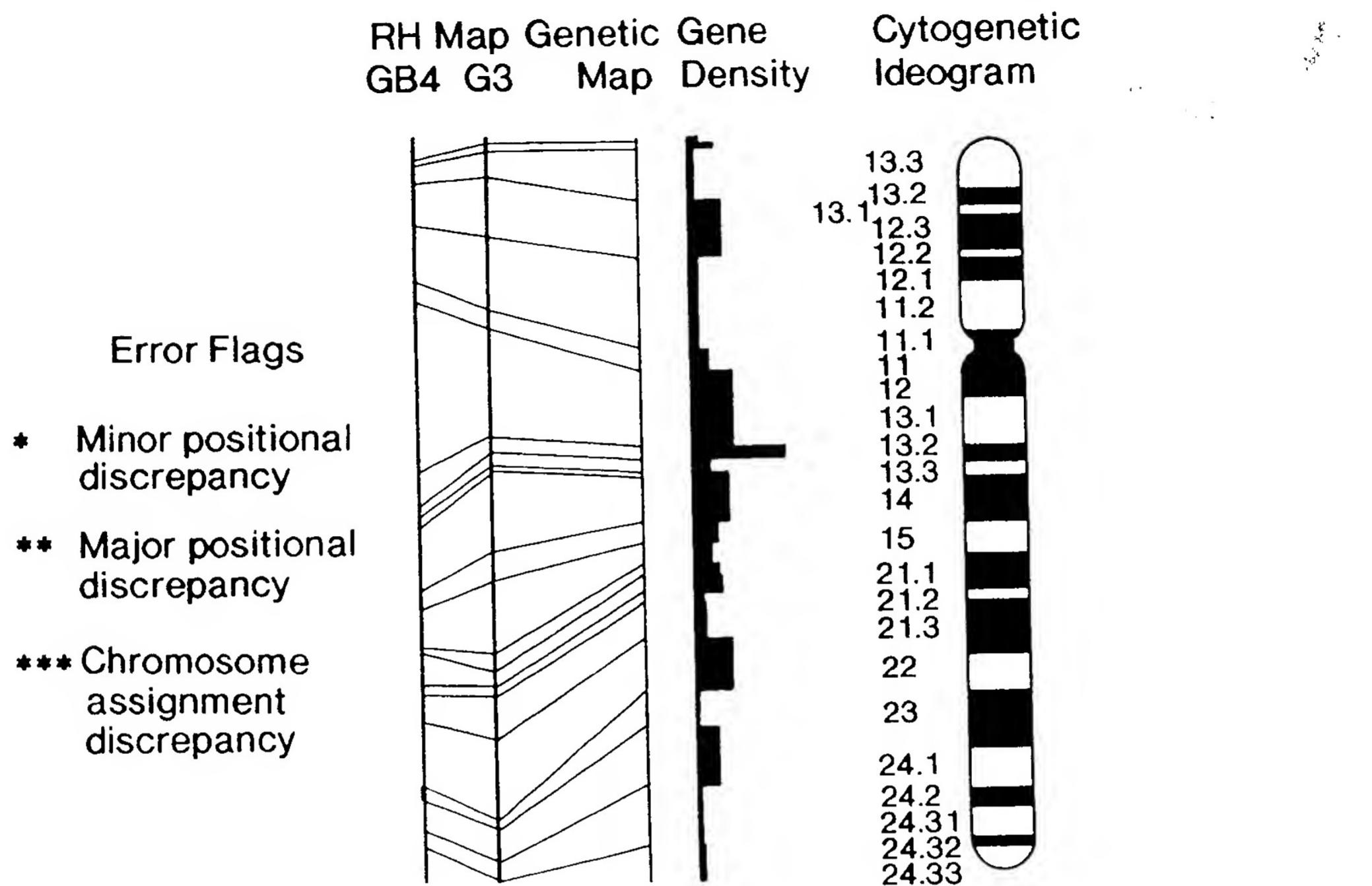
Top of interval: D12S79 (126.1 cM)
Bottom of interval: D12S366 (133.8 cM)
Genetic size of bin: 8 cM
Physical size of bin: 9 cR₃₀₀₀

FIG. 2A

 <p>126.1</p> <p>◆ 451.62 F</p> <p>454.24 P0.10</p> <p>455.39 P0.37</p> <p>455.39 P1.15</p> <p>455.70 P0.06</p> <p>455.81 P1.35</p> <p>455.86 P2.06</p> <p>456.02 P2.38</p> <p>456.34 P0.23</p> <p>456.34 P0.04 *</p> <p>456.86 P2.34</p> <p>456.86 P>3.00</p> <p>456.86 "</p> <p>456.96 P1.66 *</p> <p>456.96 P0.04</p> <p>457.17 P1.31</p> <p>457.17 P0.13</p> <p>457.17 P0.30</p> <p>457.17 P0.38</p> <p>457.17 P0.31</p> <p>457.17 P0.18</p> <p>457.17 P1.35</p> <p>457.17 "</p> <p>◆ 457.27 P>3.00 *</p> <p>457.27 P0.10 *</p> <p>457.48 P0.20</p> <p>460.94 P0.00 *</p> <p>◆ 460.94 F</p>	<p>AFM067yc5 D12S79 Microsatellite anchor marker AFM067yc5</p> <p>A009F32 KIAA0331 KIAA0331 gene product</p> <p>sts-N33343 ESTs</p> <p>SGC38179 ESTs</p> <p>stSG54526 ESTs</p> <p>stSG1522 ESTs</p> <p>sts-T56610 Homo sapiens mRNA for KIAA0875 protein, p..</p> <p>sts-R33659 EST</p> <p>sts-D29101 EST</p> <p>SGC44506 ESTs</p> <p>NIB1804 ESTs</p> <p>stSG44263 ESTs, Weakly similar to calcium-binding pr..</p> <p>stSG62560 Homo sapiens clone 24852 mRNA sequence</p> <p>sts-AA001615 ESTs</p> <p>sts-T94297 ESTs, Weakly similar to TBX2 gene [H.sapi..</p> <p>stSG54365 ESTs</p> <p>WI-21497 Homo sapiens mRNA for KIAA0875 protein, p..</p> <p>WI-20357 Homo sapiens mRNA for KIAA0875 protein, p..</p> <p>SGC31491 NOS1 nitric oxide synthase 1 (neuronal)</p> <p>RK903_904 NOS1 nitric oxide synthase 1 (neuronal)</p> <p>sts-AA007571 ESTs</p> <p>stSG46223 ESTs</p> <p>stSG58387 ESTs</p> <p>Cdalce05 Homo sapiens clone 23714 mRNA sequence</p> <p>sts-W79390 NME2 non-metastatic cells 2, protein (NM23B) exp..</p> <p>sts-Z40829 ESTs</p> <p>A005Q47 ESTs</p> <p>AFM351tb9 D12S366 Microsatellite anchor marker AFM351tb9</p>
<p>133.8</p> <p>◆ 460.94 F</p>	<p>Next interval down</p>

FIG. 2B

Chromosome 12: D12S366-D12S340



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S366 (133.8 cM)
Bottom of interval:	D12S340 (147.5 cM)
Genetic size of bin:	14 cM
Physical size of bin:	21 cR ₃₀₀₀

133.8	◆ 460.94 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9
	462.85 P1.00 *	stSG8109		ESTs
	462.85 "	sts-X75252	PBP	prostatic binding protein
	462.95 P1.04	sts-AA011374		Homo sapiens KIAA0431 mRNA, partial cds

FIG. 2C

463.77 P0.19	WI-16745		Human clone 37, 5cM region surrounding hepa..
◆ 463.77 P0.20	SGC33949	KIAA0262	KIAA0262 gene product
463.98 P0.02	A008B04		ESTs
463.98 "	stSG50309		ESTs
463.98 "	stSG49970		Homo sapiens mRNA for KIAA0875 protein, p..
463.98 P0.04	stSG27318		Human clone 23932 mRNA sequence
463.98 P0.08	R06295		EST
463.98 P1.33	sts-W56792		ESTs
464.08 P2.32	A007E48		ESTs
464.19 P1.28	A009U43		ESTs
464.29 P1.33	stSG3138		Homo sapiens mRNA for KIAA0949 protein, p..
464.39 P1.09	sts-F21636		Human DNA sequence from BAC 15E1 on chrom..
464.39 P1.13	stSG15685	KIAA0262	KIAA0262 gene product
464.39 "	RP_P0_1	RPLP0	Ribosomal protein large, P0
464.39 P1.09	stSG29626		ESTs
464.39 P1.14	stSG31407		Human DNA sequence from BAC 15E1 on chrom..
464.39 "	A001T32	PXN	paxillin
464.39 "	A001W18		H.sapiens mRNA for AMP-activated protein ..
464.39 "	WIAF-40		Human mRNA for KIAA0219 gene, partial cds
464.39 "	sts-T95105		ESTs
464.39 "	Cda0id01		ESTs
464.39 P1.13	stSG31431		ESTs, Moderately similar to (defline not a..
◆ 464.39 " *	WI-13177		Homo sapiens clone 23714 mRNA sequence
464.39 "	IB1092		Homo sapiens clone 23714 mRNA sequence
464.39 "	T79466		ESTs
464.39 P1.18	stSG48379		ESTs
464.45 P1.05	KIAA0219		Human mRNA for KIAA0219 gene, partial cds
464.45 "	stSG40392		ESTs
464.45 "	stSG31586		H.sapiens mRNA for AMP-activated protein ..
◆ 464.49 P0.21	A006F12	KIAA0152	KIAA0152 gene product
464.49 P0.25	sts-AA002185	PXN	paxillin
464.49 P0.10	stSG48442		ESTs
464.49 "	sts-T16456		ESTs
464.49 "	stSG62260		ESTs

FIG. 2D

	464.49 "	NIB1331		ESTs
	464.49 "	WI-15518		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49 "	WIAF-1058		ESTs, Moderately similar to unknown [H.sap..
	464.49 "	SGC34758		ESTs
	464.49 "	WI-19738		Homo sapiens mRNA for KIAA0787 protein, p..
	464.49 "	IB383		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49 "	SGC32343		ESTs
	464.79 P0.96	SGC33521		ESTs
	464.79 P0.96 *	X58965	NME2	non-metastatic cells 2, protein (NM23B) exp..
	465.20 P0.20	sts-H10302		ESTs
◆	465.38 P0.85	A007E11	KIAA0262	KIAA0262 gene product
	465.41 P0.81	A007I44	RPLP0	ribosomal protein, large, P0
	465.41 "	stSG22726		EST
	465.41 "	WI-17776		ESTs
	465.41 "	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41 "	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41 P0.77	stSG4775	SFRS9	splicing factor, arginine-serine-rich 9
	465.41 "	A002J47		ESTs, Weakly similar to heat shock protein..
	465.41 P0.80	stSG46660		EST
	465.51 P0.75	stSG41086	PXN	paxillin
	465.51 P0.83	stSG52121		ESTs
	465.91 P0.01	WI-16071		ESTs
	465.91 P0.00	WI-13962		H.sapiens mRNA for AMP-activated protein ..
	466.62 P0.00	sts-AA011220	SFRS9	splicing factor, arginine-serine-rich 9
	466.71 P0.00	stSG4712		ESTs, Weakly similar to homology with o251..
	466.91 P0.01	WI-15135		Homo sapiens mRNA for KIAA0787 protein, p..
	466.91 P0.01	D12S2088	TCF1	transcription factor 1, hepatic; LF-B1, hep..
	467.01 P0.01	stSG52567		ESTs
135.1	467.11 F	AFM123xh2	D12S86	Microsatellite marker AFM123xh2
135.1	467.11 P0.01	AFM299zd5	D12S349	Microsatellite marker AFM299zd5
	467.11 P0.01	AFM123xh2		Unknown
137.5	◆ 467.21 P0.02	AFM220zf4	D12S321	Microsatellite marker AFM220zf4
	467.21 P0.02	sts-W73277	SFRS9	splicing factor, arginine-serine-rich 9
	467.21 P0.02	stSG8721		EST

FIG. 2E

467.21 "	stSG44224		ESTs
467.21 "	stSG49978		H.sapiens mRNA for AMP-activated protein ..
◆ 467.21 "	stSG31862		Homo sapiens HSPC004 mRNA, complete cds
467.21 "	stSG47820		ESTs
467.21 "	Bdac4h06	KIAA0262	KIAA0262 gene product
467.21 "	stSG15021		ESTs
467.21 "	A002B13	SFRS9	splicing factor, arginine-serine-rich 9
◆ 467.21 "	H50549	KIAA0262	KIAA0262 gene product
467.21 P0.03	SGC35167		EST
467.21 P0.03	WI-19637		H.sapiens mRNA for AMP-activated protein ..
467.21 P0.02	WIAF-607		Unknown
467.31 P0.02	WI-16997	RPLP0	ribosomal protein, large, P0
468.93 P0.85	SGC31344		EST
469.13 P0.90	A007C39	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 ..
469.13 P0.14	stSG35104		ESTs
469.13 "	A006Q41		Unknown
469.23 P0.18	sts-Y07684	P2RX4	purinergic receptor P2X, ligand-gated ion c..
469.33 P0.93	stSG8506		ESTs, Moderately similar to unknown [H.sap..]
469.33 "	R01708		EST
469.33 "	stSG54819	HCALB_BR	calbrain
469.33 "	A001Z45		ESTs, Highly similar to (defline not avail..)
469.33 "	stSG35318		ESTs, Weakly similar to fos39554 1 [H.sapi..]
469.33 "	stSG63173		EST
469.33 "	stSG31374	OASL	2'-5'oligoadenylate synthetase-like
469.42 P1.01	WI-16068		EST
469.44 P0.23	stSG1961		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62627		EST
469.44 "	stSG36007		Homo sapiens full length insert cDNA clone..
469.44 "	stSG39281	P2RX7	purinergic receptor P2X, ligand-gated ion c..
469.44 "	stSG2554		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62591		ESTs
◆ 469.54 P1.03	A006N38	KIAA0152	KIAA0152 gene product
469.62 P1.03	sts-N34573		ESTs
469.62 P1.03	sts-N58045		ESTs

FIG. 2F

469.62 P1.04		WI-13224		EST
469.83 P1.12		SGC34424		ESTs
469.93 P1.14		stSG3875	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.14 P1.17		stSG52516		ESTs, Weakly similar to (defline not avail..)
470.24 P1.32		D0S1735E		ESTs
470.24 P1.12		WI-6178		ESTs
470.32 P1.25		sts-U29895		Unknown
470.32 P1.24		WI-19611	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.43 P1.29		stSG52094		ESTs
470.63 P1.38		A004O17		ESTs
◆ 470.77 P1.32	**	SGC33451		ESTs, Weakly similar to rhoHP1 [H.sapiens..]
◆ 470.84 P1.35	**	sts-X64838	RSN	restin (Reed-Steinberg cell-expressed inter..)
470.84 P1.52		WI-13062		Homo sapiens mRNA, expressed in fibroblast..
471.27 P1.60		sts-R99269		EST
471.37 P1.70		stSG1991		ESTs
471.37 "		stSG15859		Homo sapiens full length insert cDNA YQ02..
471.58 P1.78		stSG29729		ESTs, Weakly similar to (defline not avail..)
471.58 P1.37		WI-16979		ESTs
471.65 P1.39		WI-17693		EST
471.80 P1.29		WI-22060		ESTs
471.90 P>3.00		stSG8210		ESTs, Moderately similar to neuronal threa..
471.90 "		WI-17956		EST
471.90 "		WI-20969		Homo sapiens mRNA for KIAA0867 protein, c..
471.90 "		stSG47029		ESTs
471.90 "		stSG47647		EST
471.90 "		sts-W45376		Homo sapiens mRNA for KIAA0867 protein, c..
◆ 471.90 "	**	WI-6021	RSN	restin (Reed-Steinberg cell-expressed inter..)
471.90 "		NIB962		ESTs
471.90 "		A009E34		ESTs, Moderately similar to neuronal threa..
471.90 "		sts-T17477		ESTs
472.08 P1.49		sts-X89984		H.sapiens mRNA for BCL7A protein
472.12 P>3.00		SGC34693		EST
472.12 P>3.00		A009O01		ESTs, Weakly similar to neuronal thread pr..
472.29 P>3.00		stSG47084		ESTs

FIG. 2G

472.40 P>3.00	stSG58209	EEF1D	eukaryotic translation elongation factor 1 d..
472.40 P>3.00	AA213821	EEF1D	eukaryotic translation elongation factor 1 d..
472.61 P>3.00	A002R44		Unknown
472.61 P>3.00	SGC35850	EEF1D	eukaryotic translation elongation factor 1 d..
472.72 P0.01	sts-H98108		ESTs
472.97 P>3.00	WI-6239		ESTs
473.04 P>3.00	sts-H75490		ESTs
◆ 473.58 P>3.00 **	WI-14983	RSN	restin (Reed-Steinberg cell-expressed inter..
474.01 P>3.00	stSG8610		ESTs
474.01 P>3.00	stSG47080		ESTs
474.38 P2.18	stSG8686		ESTs, Weakly similar to similar to pre-mRN..
474.38 P2.25	stSG26358		ESTs, Weakly similar to similar to pre-mRN..
474.38 "	stSG29931		ESTs
474.38 "	WI-17926		ESTs
474.38 "	WI-12790		ESTs, Weakly similar to MULTIDRUG RESI..
474.38 "	1834		EST
474.38 P2.26	sts-X98258	MPP-9	M phase phosphoprotein 9
474.38 P2.39	stSG40753		ESTs
474.64 P>3.00	A004D47		ESTs, Highly similar to There are three pu..
474.64 P>3.00	sts-N23129	MPP-9	M phase phosphoprotein 9
474.75 P2.41	sts-AA040696		ESTs
474.81 P2.37	sts-AA022496		ESTs
474.81 P2.28	stSG46930	MPP-9	M phase phosphoprotein 9
474.97 P>3.00	WI-20552	DRP	density-regulated protein
475.02 P>3.00	SGC30324		ESTs
475.07 P>3.00	D10923	HM74	putative chemokine receptor; GTP-binding pr..
475.07 P>3.00	stSG2418	DOC1	Deleted in oral cancer-1
475.07 "	stSG21321		ESTs
475.07 "	stSG53515	MPP-9	M phase phosphoprotein 9
475.07 P>3.00	SGC31687	DOC1	Deleted in oral cancer-1
475.07 P>3.00	WIAF-214	HM74	putative chemokine receptor; GTP-binding pr..
475.13 P0.79	sts-W93806		ESTs
475.13 P2.13	stSG48145		ESTs
475.18 P2.34	A003B12		Homo sapiens full length insert cDNA clone..

FIG. 2H

	475.18 P>3.00	WI-22211	Homo sapiens full length insert cDNA clone..
	475.18 P2.08	stSG48093	ESTs
	475.18 "	A004P27	ESTs, Weakly similar to MULTIDRUG RESI..
	475.35 P2.10	stSG9904	ESTs
	475.40 P0.45	sts-AA024696	ESTs
	475.51 P>3.00	stSG53793	ESTs
	476.10 P>3.00	Bda98d05	Homo sapiens full length insert cDNA clone..
	476.21 P>3.00	sts-H24468	ESTs
	476.21 P>3.00	sts-N94741	ESTs
	476.64 P0.28	stSG22488	ESTs
	476.85 P0.36	stSG44909	ESTs
	477.06 P0.10	stSG54797	ESTs
	477.27 P1.33	stSG48099	ESTs
	477.37 P0.09 *	sts-AA028894	Homo sapiens silencing mediator of retinoic..
	477.80 P1.44	stSG52727	EST
	477.80 "	U44799	Human U1-snRNP binding protein homolog mR..
	477.80 "	WI-15963	ESTs
	477.80 "	stSG53886	ESTs, Weakly similar to neuronal thread pr..
	478.74 P0.01	WIAF-364	ESTs
	479.01 P0.21	WI-21080	ESTs
	479.13 P0.19	A009B29	ESTs
	479.33 P0.22	A006F32	EIF2B1 eukaryotic translation initiation factor 2B..
	479.33 P0.19	WIAF-449	EIF2B1 eukaryotic translation initiation factor 2B..
	479.33 P0.19 *	WI-15890	H.sapiens mRNA for transmembrane protein r..
	479.55 P0.20 *	stSG349	H.sapiens mRNA for transmembrane protein r..
	479.55 "	*	BDKRB2 bradykinin receptor B2
	479.55 "	stSG42540	ESTs
	479.55 "	sts-N26791	ESTs
	479.55 "	stSG53943	ESTs
	479.55 "	stSG49468	EST
145.7	479.74 P0.16	AFM294ze9	D12S342 Microsatellite marker AFM294ze9
	481.46 P0.00	sts-AA007694	EST
147.5	◆ 481.56 F	AFM294xg1	D12S340 Microsatellite anchor marker AFM294xg1

Next interval down

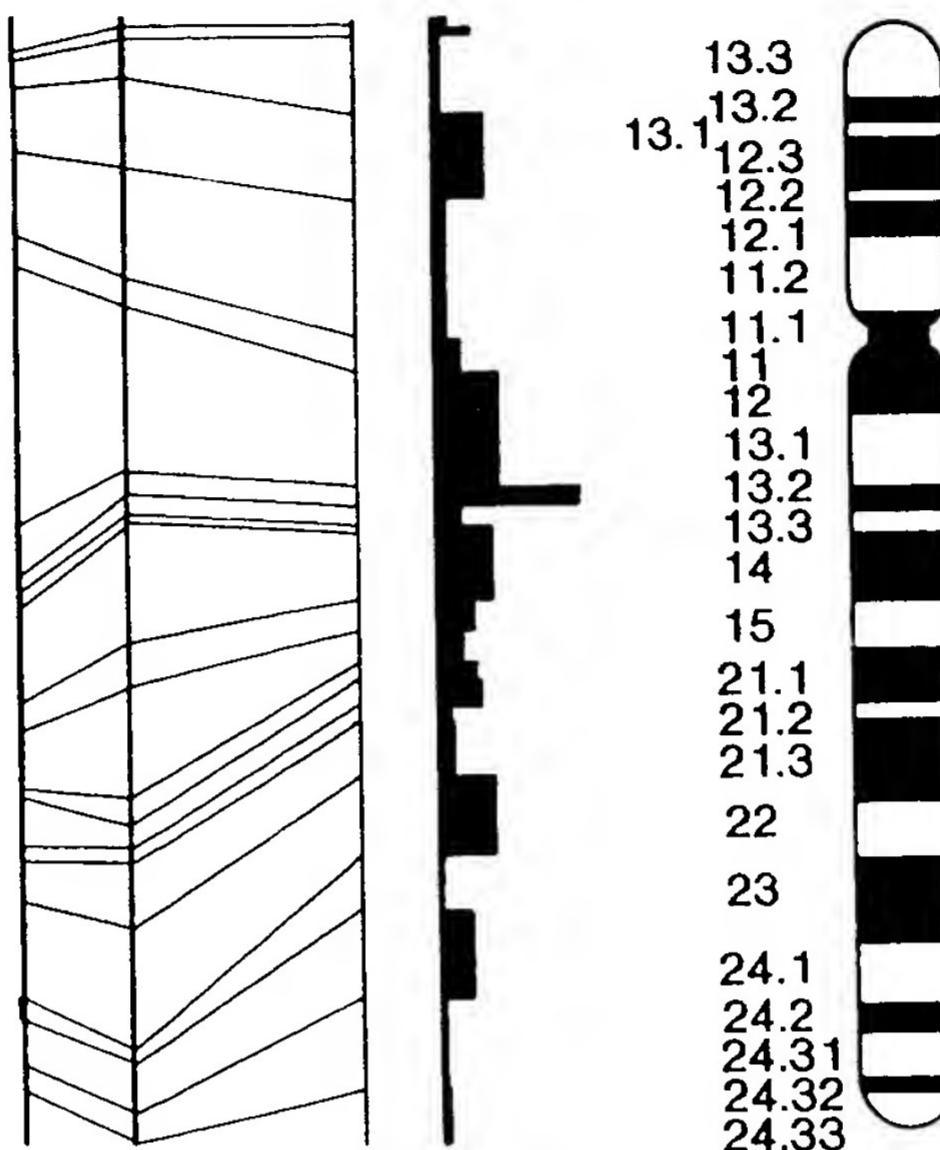
FIG. 2I

Chromosome 12: D12S340-D12S97

RH Map GB4	Genetic G3	Gene Map	Gene Density	Cytogenetic Ideogram
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Error Flags

- * Minor positional discrepancy
- ** Major positional discrepancy
- *** Chromosome assignment discrepancy



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S340 (147.5 cM)
Bottom of interval:	D12S97 (160.9 cM)
Genetic size of bin:	13 cM
Physical size of bin:	13 cR ₃ 000

147.5	◆ 481.56 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1
	481.66 P0.00	SGC31838		ESTs
	483.18 P0.70	stSG48255		ESTs
	483.58 P0.69	stSG47315		ESTs

Next interval up

FIG. 2J

483.87 P0.83	stSG47707		ESTs
484.70 P0.93	stSG4060		ESTs
484.70 "	stSG62390	GTF2H3	general transcription factor IIH, polypepti..
484.70 "	stSG42994		ESTs
484.73 P0.74	stSG46906		ESTs
484.80 P0.91	A004X33		ESTs
484.91 P1.11	stSG3211		ESTs, Weakly similar to B-cell growth fact..
484.91 " *	sts-Z41302	BDKRB2	bradykinin receptor B2
484.91 " *	sts-Z41302	BDKRB2	bradykinin receptor B2
484.91 "	sts-T58259		ESTs, Weakly similar to B-cell growth fact..
484.91 "	stSG52737		ESTs
484.91 "	Bda03b10	UBC	ubiquitin C
484.91 "	stSG1936	CD36L1	CD36 antigen (collagen type I receptor, thr..
484.91 "	sts-AA017225		ESTs
484.91 P1.15	WI-12212		ESTs
485.12 P1.18	A004F14		ESTs
485.12 P1.18	SGC31333		ESTs
485.23 P1.21 *	WI-12482	BDKRB2	bradykinin receptor B2
485.23 P1.07	sts-AA017698		ESTs
485.33 P1.22	WI-12422		ESTs
485.51 P1.18	stSG42398		EST
485.64 P1.04	sts-AA009669		ESTs
486.07 P2.50	stSG21539		EST
486.13 P1.44	WI-12439		EST
486.34 P1.26	sts-W31616	UBC	ubiquitin C
486.38 P>3.00	stSG54715		ESTs
486.76 P1.64 *	WI-6921		H.sapiens mRNA for transmembrane protein r..
487.08 P>3.00	WI-13120		Human mRNA for KIAA0318 gene, partial cds
487.23 P>3.00	stSG54353		ESTs
487.23 P>3.00	stSG22703		EST
487.28 P>3.00	stSG62698		ESTs
487.28 P>3.00 *	sts-D60472		Homo sapiens silencing mediator of retinoic..
487.28 P>3.00	stSG36097		ESTs
487.33 P1.36	sts-U37146		Homo sapiens silencing mediator of retinoic..

FIG. 2K

	487.50 P>3.00	stSG9807	ESTs
	487.50 P>3.00	stSG15434	ESTs
	487.60 P>3.00	stSG53251	ESTs
	487.60 P>3.00	stSG30525	SRRP129 SC35-interacting protein 1
	487.60 P>3.00	stSG46424	ESTs
	487.70 P>3.00	A007A34	ESTs
154.4	487.75 P2.00	AFMa197zd9	D12S1609 Microsatellite marker AFMa197zd9
	487.75 P2.02	A006D44	ESTs
	487.80 P>3.00	SGC30248	ESTs, Weakly similar to peptide/histidine ..
	488.07 P1.68	stSG6320	Homo sapiens clone 24617 mRNA sequence
	488.07 P1.66	stSG6305	Homo sapiens clone 24790 mRNA sequence
	488.07 P0.02	sts-N20163	Homo sapiens full length insert cDNA clone..
	488.12 P>3.00	stSG60065	ESTs
	488.12 P>3.00	stSG47723	ESTs
	488.44 P1.59	stSG3292	Homo sapiens clone 24790 mRNA sequence
	488.44 P0.03	WIAF-856	EST, Weakly similar to reverse transcripta..
	488.65 P1.54	WI-12272	Homo sapiens clone 24790 mRNA sequence
	488.65 P1.82	stSG52343	ESTs
	488.82 P1.80	stSG16387	CPN2 carboxypeptidase N, polypeptide 2, 83kD
	488.97 P1.80	SGC31722	ESTs
	489.07 P0.06	stSG54325	ESTs
	489.07 P>3.00	stSG63473	ESTs
160.9	◆ 489.07 P>3.00	AFMa123xe1	D12S367 Microsatellite marker AFMa123xe1
	489.14 P0.17	sts-T81113	ESTs
	489.29 P0.05	sts-AA025438	EST
	489.50 P1.37	*** Cdalad08	ESTs
	489.50 P0.05	WI-15018	ESTs
	489.50 P1.50	WI-18492	ESTs
	489.57 P1.48	WI-16177	Homo sapiens androgen receptor associated p..
	489.67 P1.44	stSG53307	ESTs
	489.71 P1.43	stSG53541	Homo sapiens hiwi mRNA, partial cds
	489.71 P1.43	stSG9546	Homo sapiens clone 24617 mRNA sequence
	489.89 P1.56	A006O16	ESTs
	490.10 P1.42	H64839	EST

FIG. 2L

160.9 490.20 P.05 stSG43910 SFRS8 splicing factor, arginine/serine-rich 8 (sup..)
 ◆ 494.19 F AFM210zd6 D12S97 Microsatellite anchor marker AFM210zd6
↓ Next interval down

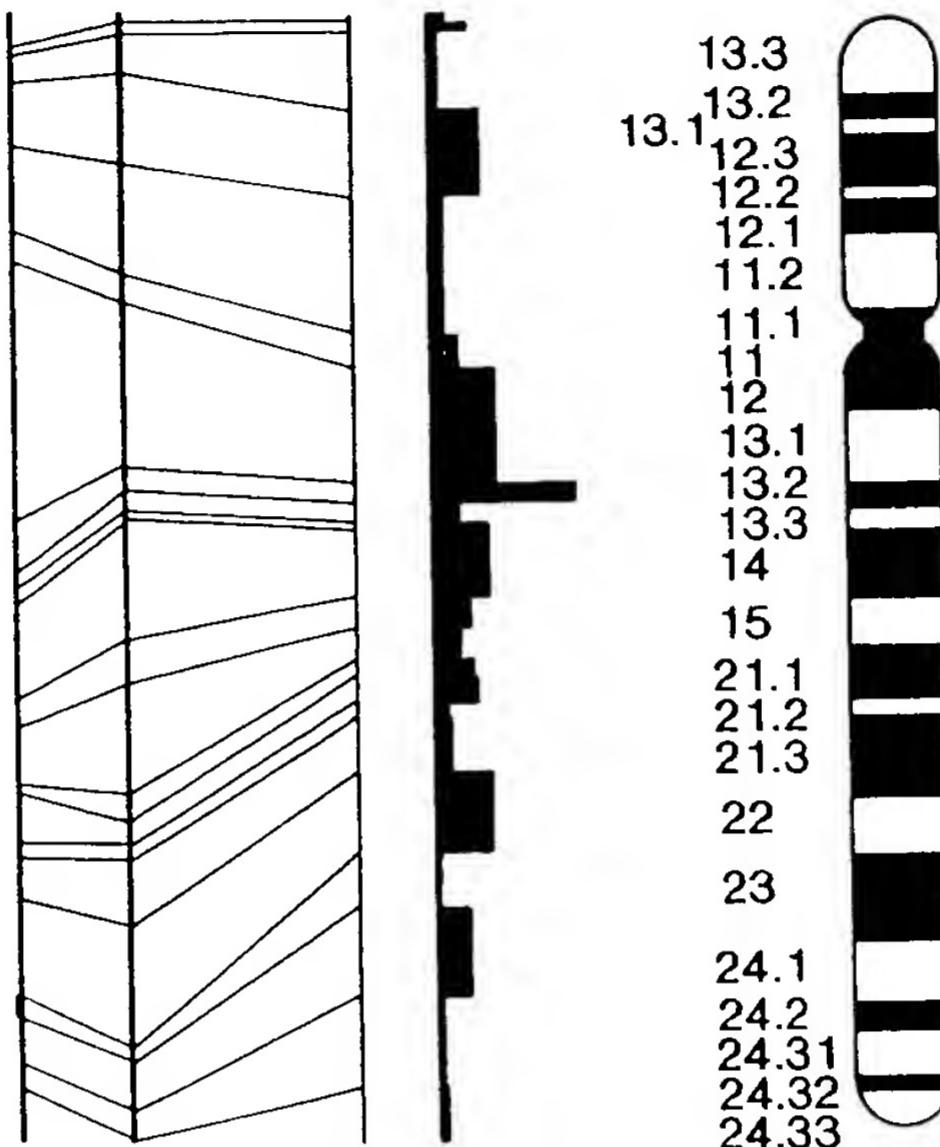
FIG. 2M

Chromosome 12: D12S97-qTEL

RH Map GB4	Genetic G3	Gene Map	Gene Density	Cytogenetic Ideogram
---------------	---------------	-------------	-----------------	-------------------------

Error Flags

- * Minor positional discrepancy
- ** Major positional discrepancy
- *** Chromosome assignment discrepancy



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S97 (160.9 cM)
Bottom of interval:	chr12_qTEL (169.1 cM)
Genetic size of bin:	8 cM
Physical size of bin:	172 cR3000

160.9	◆ 494.19 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6
		stSG53600		ESTs, Weakly similar to peptide/histidine ..
	498.06 P0.02			
	499.71 P1.73	stSG3357		ESTs
165.7	499.71 "	AFM295ye9	D12S343	Microsatellite marker AFM295ye9

FIG. 2N

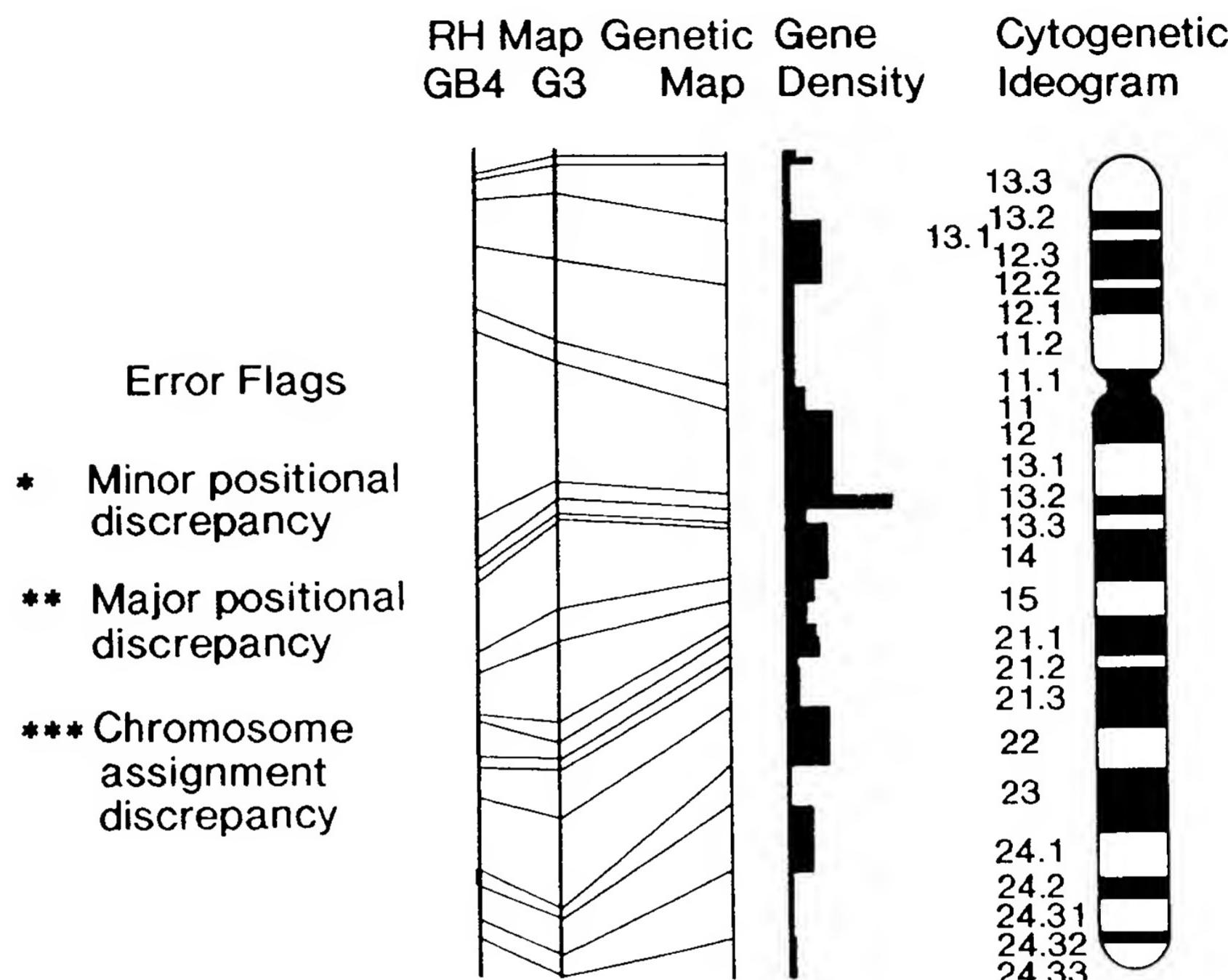
499.71 P1.72	stSG30906		ESTs
499.71 "	stSG43796	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.71 P1.71	sts-X89576	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.92 P>3.00	stSG43769		ESTs
500.50 P1.88	stSG26056		ESTs
500.50 P2.33	SGC30786	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG1702		Homo sapiens CAGH32 mRNA, partial cds
500.61 "	sts-N59820		ESTs
500.61 "	stSG42115	KIAA0331	KIAA0331 gene product
500.61 "	IB2452	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 "	stSG52521		ESTs
500.61 "	FB9F8		ESTs, Weakly similar to PUTATIVE ATP-D..
500.61 "	AA252357		ESTs
500.61 "	stSG4720		Homo sapiens pseudouridine synthase 1 (PUS..
500.61 "	sts-AA001424	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG31443		ESTs
500.61 P>3.00	stSG49622	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 P2.49	stSG50559		ESTs
501.04 P1.10	stSG54842		ESTs
501.04 P2.03	A008Y05		Unknown
501.89 P2.18	stSG39493		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	A002A44		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	sts-H94865		EST
501.99 P>3.00	R50113		ESTs
502.10 P1.75	stSG48386		ESTs
502.10 "	stSG50504		ESTs
502.63 P0.06	A006R19		ESTs
502.63 P1.06	WIAF-864		ESTs
502.94 P1.51	stSG54813		ESTs, Weakly similar to peroxisome membran..
503.04 P1.42	A004B47		ESTs, Highly similar to DNA polymerase ep..
503.25 P0.28	stSG27206		ESTs
503.25 "	stSG40199		Homo sapiens mRNA for KIAA0692 protein, p..
503.46 P0.23	stSG8935		ESTs
504.68 P0.69	stSG4731		Homo sapiens mRNA for KIAA0692 protein, p..

	504.68 "	A005Q05	ESTs
	504.68 "	stSG8142	ESTs, Highly similar to DNA polymerase ep..
169.1	506.39 F	AFM310vd5 D12S357	Microsatellite marker AFM310vd5
	506.39 P0.02	A005X42	Homo sapiens mRNA for KIAA0692 protein, p..
	508.59 P0.78	Cda18g06	ESTs
	◆ 508.59 P0.78 **	Cda1jf08	Homo sapiens mRNA for GCP170, complete cd..
	508.59 P0.54	R39599	ESTs
	509.98 P0.10	stSG31494 ZNF140	zinc finger protein 140 (clone pHZ-39)
	509.98 P0.16	stSG40222	ESTs
	509.98 "	sts-R55615	ESTs, Weakly similar to zinc finger protei..
	509.98 "	sts-R02295	ESTs
	509.98 "	sts-R81342	ESTs
	511.20 F	TEL-12q82	Marker TEL-12q82
	512.81 P0.20	sts-H65839	ESTs, Weakly similar to transformation-rel..
	514.97 P0.36	stSG46141	ESTs, Weakly similar to zinc finger protei..
	514.97 P0.90	stSG52998	ESTs
	519.10 P1.77	A008W21 CYP51	cytochrome P450, 51 (lanosterol 14-alpha-de..
	519.54 P0.81	stSG52716	ESTs

TELOMERE

FIG. 2P

Chromosome 12: D12S79-D12S366



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

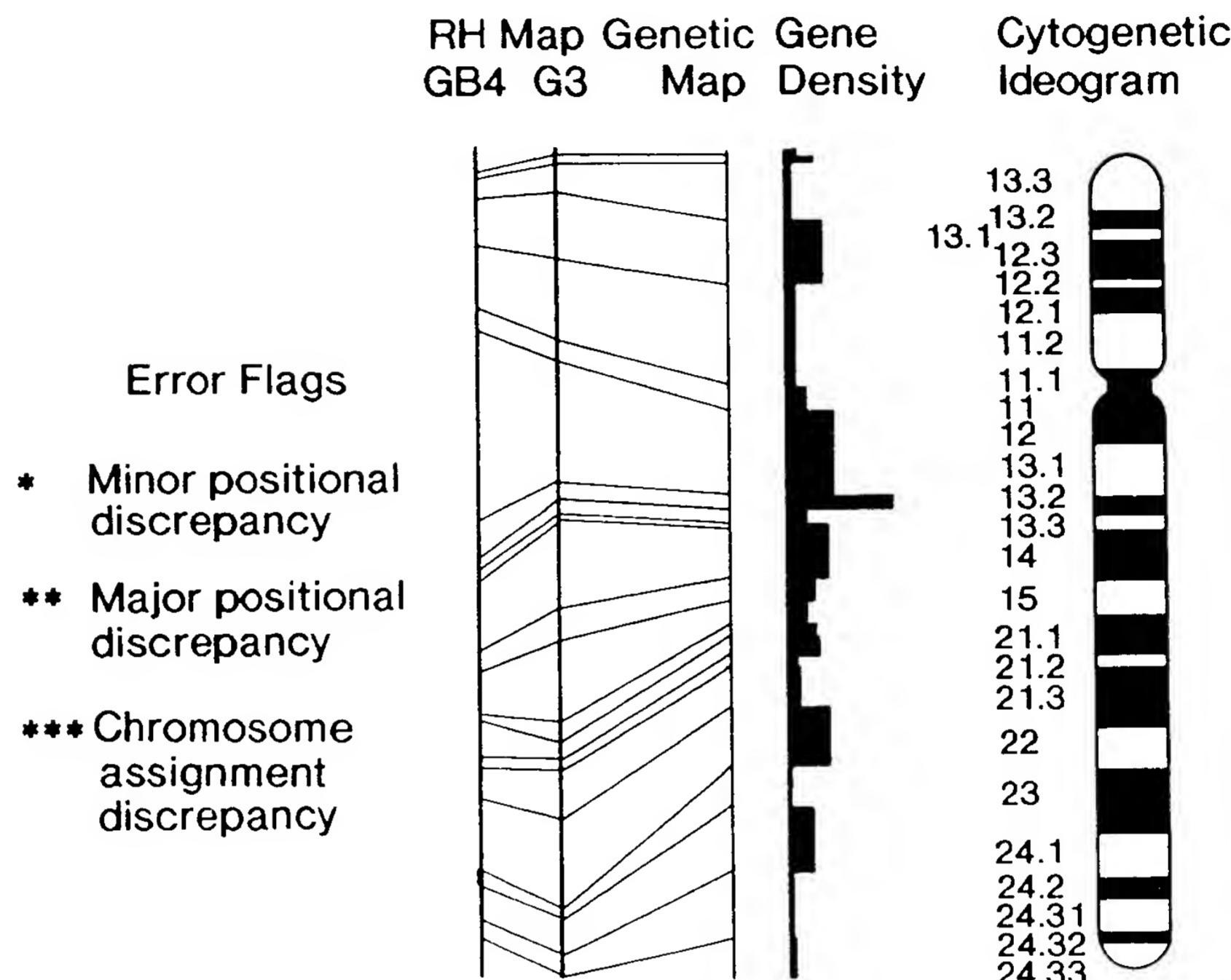
Top of interval:	D12S79 (126.1 cM)
Bottom of interval:	D12S366 (133.8 cM)
Genetic size of bin:	8 cM
Physical size of bin:	63 cR ₁₀₀₀₀

FIG. 3A

		◆	4955 F	AFM067yc5 D12S79	Microsatellite anchor marker AFM067yc5 (SHGC-692)
126.1	=	◆	4988 F	AFMa067wel D12S1718	Microsatellite marker AFMa067wel (SHGC-20..)
129.2		◆	5007 F *	SHGC-2657	Homo sapiens clone 23714 mRNA sequence
		◆	5014 F *	SHGC-2653	Homo sapiens clone 23714 mRNA sequence
133.8	=	◆	5018 F	AFM351tb9 D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)
		◆			
		↓	Next interval down		
		↑	Next interval up		

FIG. 3B

Chromosome 12: D12S366-D12S340



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

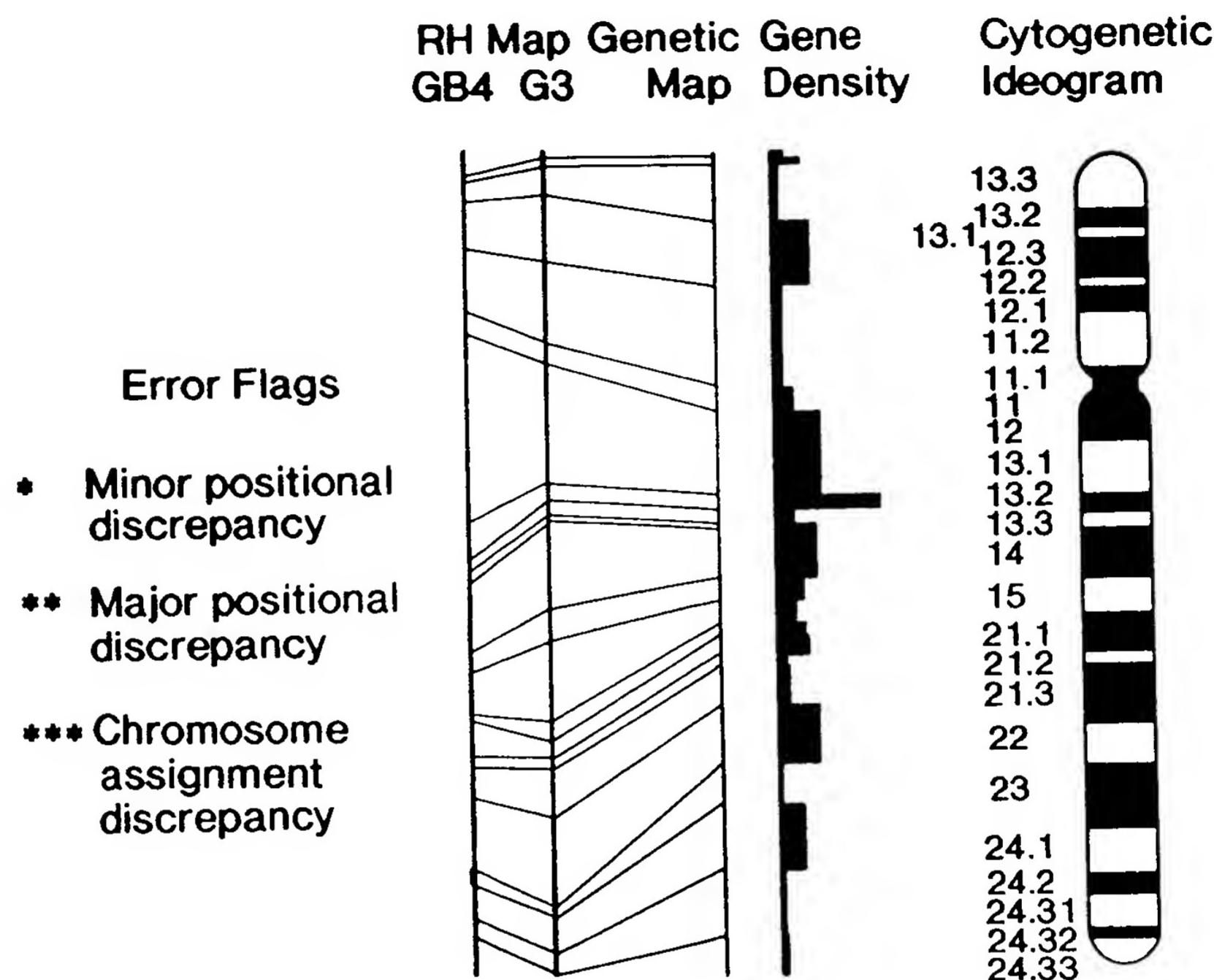
Top of interval:	D12S366 (133.8 cM)
Bottom of interval:	D12S340 (147.5 cM)
Genetic size of bin:	14 cM
Physical size of bin:	261 cR ₁₀₀₀₀

FIG. 3C

			↑	Next interval up
133.8	◆ 5018 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)
135.1	5047 F	AFMa225xe5	D12S1619	Microsatellite marker AFMa225xe5 (SHGC-20..)
	◆ 5085 F	SHGC-33949	KIAA0262	KIAA0262 gene product
	◆ 5089 F	SHGC-10488	KIAA0152	KIAA0152 gene product
	◆ 5093 F	SHGC-10346		Homo sapiens HSPC004 mRNA, complete cds
	◆ 5098 F	SHGC-13898		Homo sapiens HSPC004 mRNA, complete cds
137.5	◆ 5163 F	AFM220zf4	D12S321	Microsatellite marker AFM220zf4 (SHGC-212..)
	5199 F	SHGC-11702		ESTs
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)
		↓		Next interval down

FIG. 3D

Chromosome 12: D12S340-D12S97



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S340 (147.5 cM)
Bottom of interval: D12S97 (160.9 cM)
Genetic size of bin: 13 cM
Physical size of bin: 151 cR₁₀₀₀₀

FIG. 3E

					Next interval up
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)	
148.3	5288 F	AFM234tb10	D12S324	Microsatellite marker AFM234tb10 (SHGC-21..)	
154.4	5316 F	AFMb350zb5	D12S1679	Microsatellite marker AFMb350zb5 (SHGC-20..)	
149.5	5358 F	AFM198wh2	D12S307	Microsatellite marker AFM198wh2 (SHGC-211..)	
157.2	5393 F	AFMb301we5	D12S1659	Microsatellite marker AFMb301we5 (SHGC-20..)	
160.9	◆ 5415 F	AFMa123xe1	D12S367	Microsatellite marker AFMa123xe1 (SHGC-21..)	
160.9	◆ 5430 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6 (SHGC-372)	

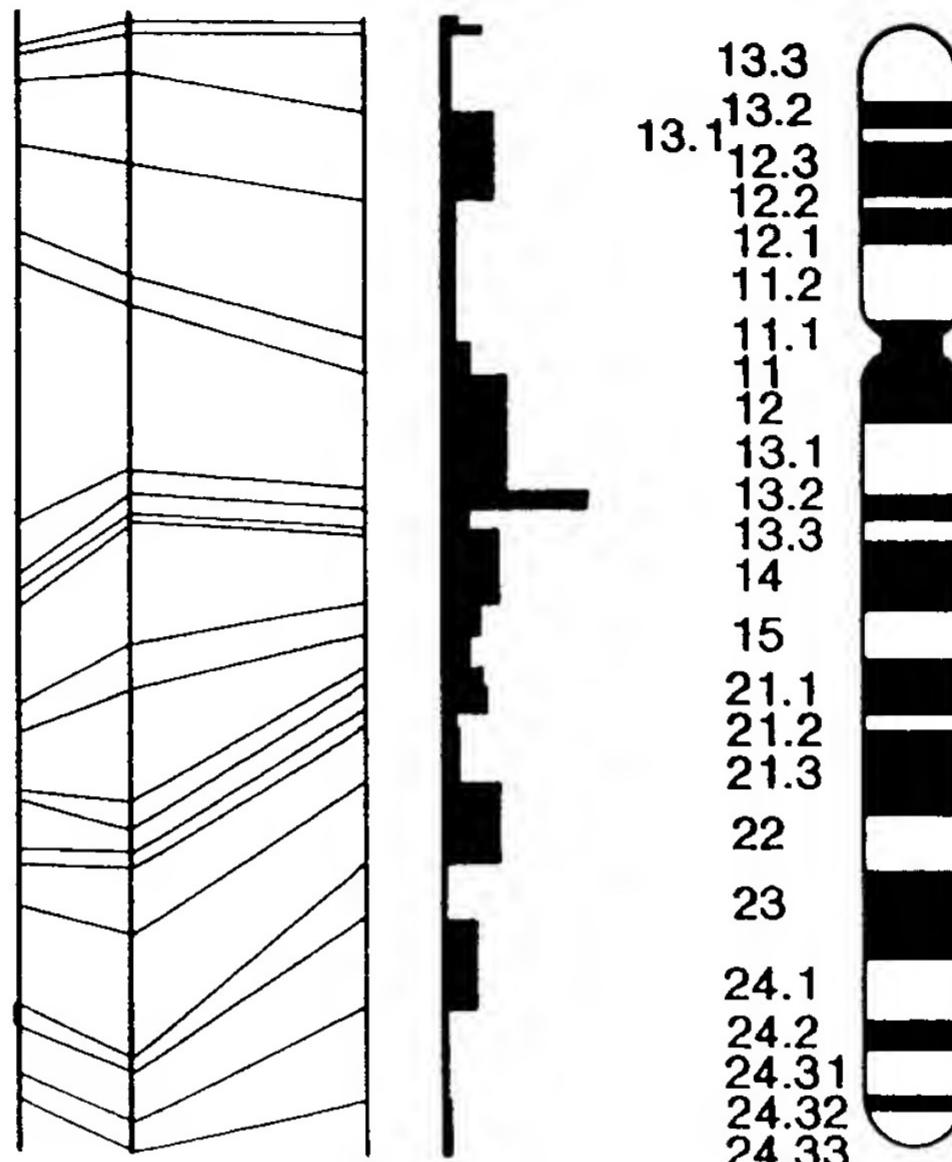
FIG. 3F

Chromosome 12: D12S97-qTEL

RH Map GB4	Genetic G3	Gene Map	Cytogenetic Density	Ideogram
---------------	---------------	-------------	------------------------	----------

Error Flags

- * Minor positional discrepancy
- ** Major positional discrepancy
- *** Chromosome assignment discrepancy



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S97 (160.9 cM)
Bottom of interval: chr12_qTEL (169.1 cM)
Genetic size of bin: 8 cM
Physical size of bin: ~ 4429 cR₁₀₀₀₀

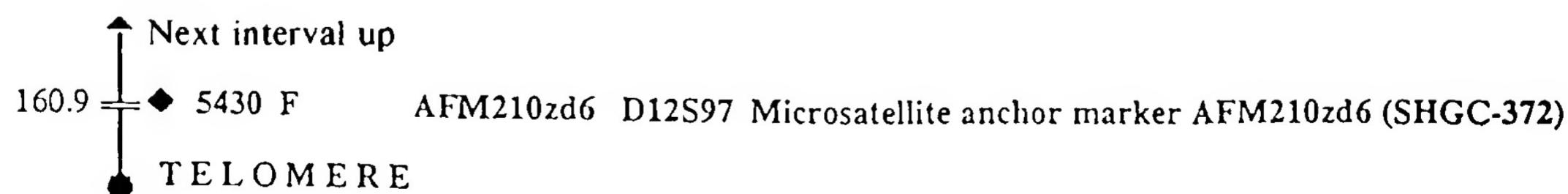


FIG. 3G

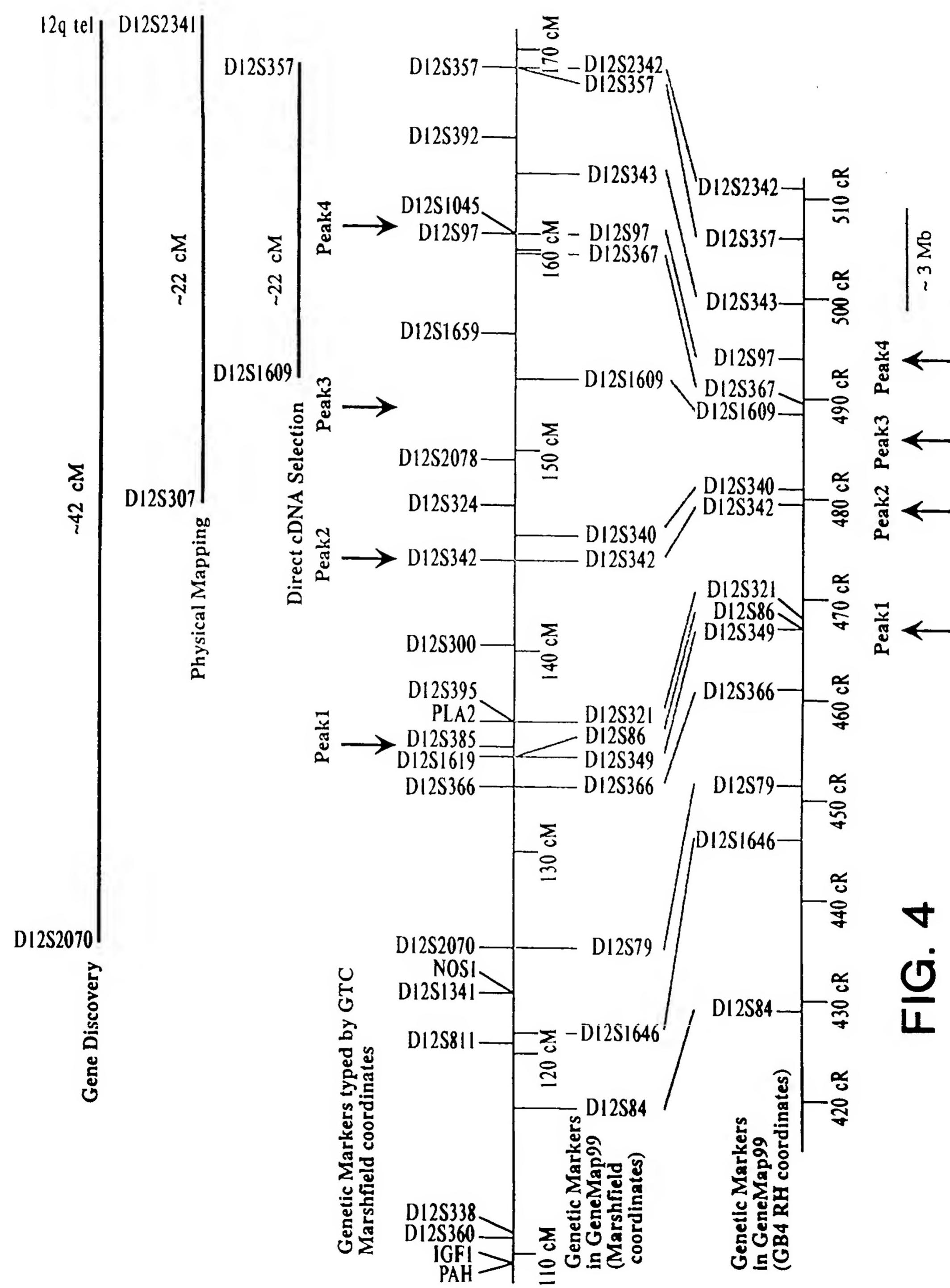
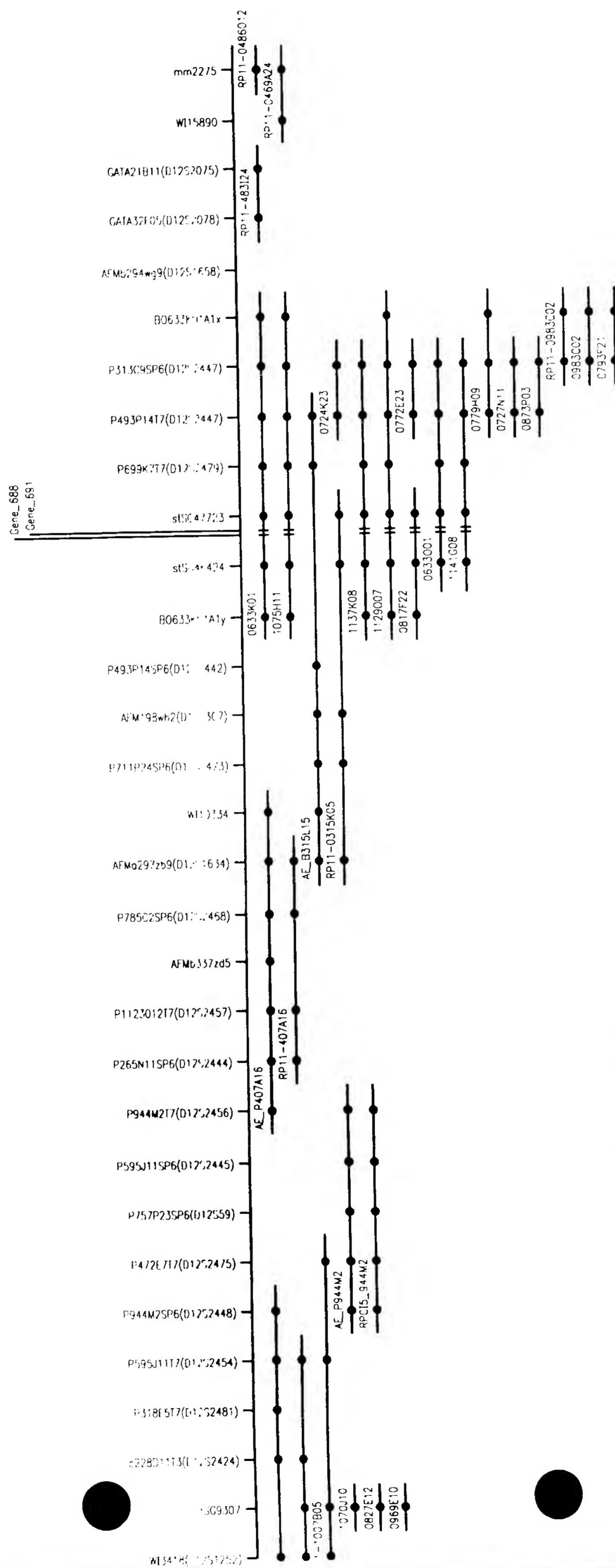
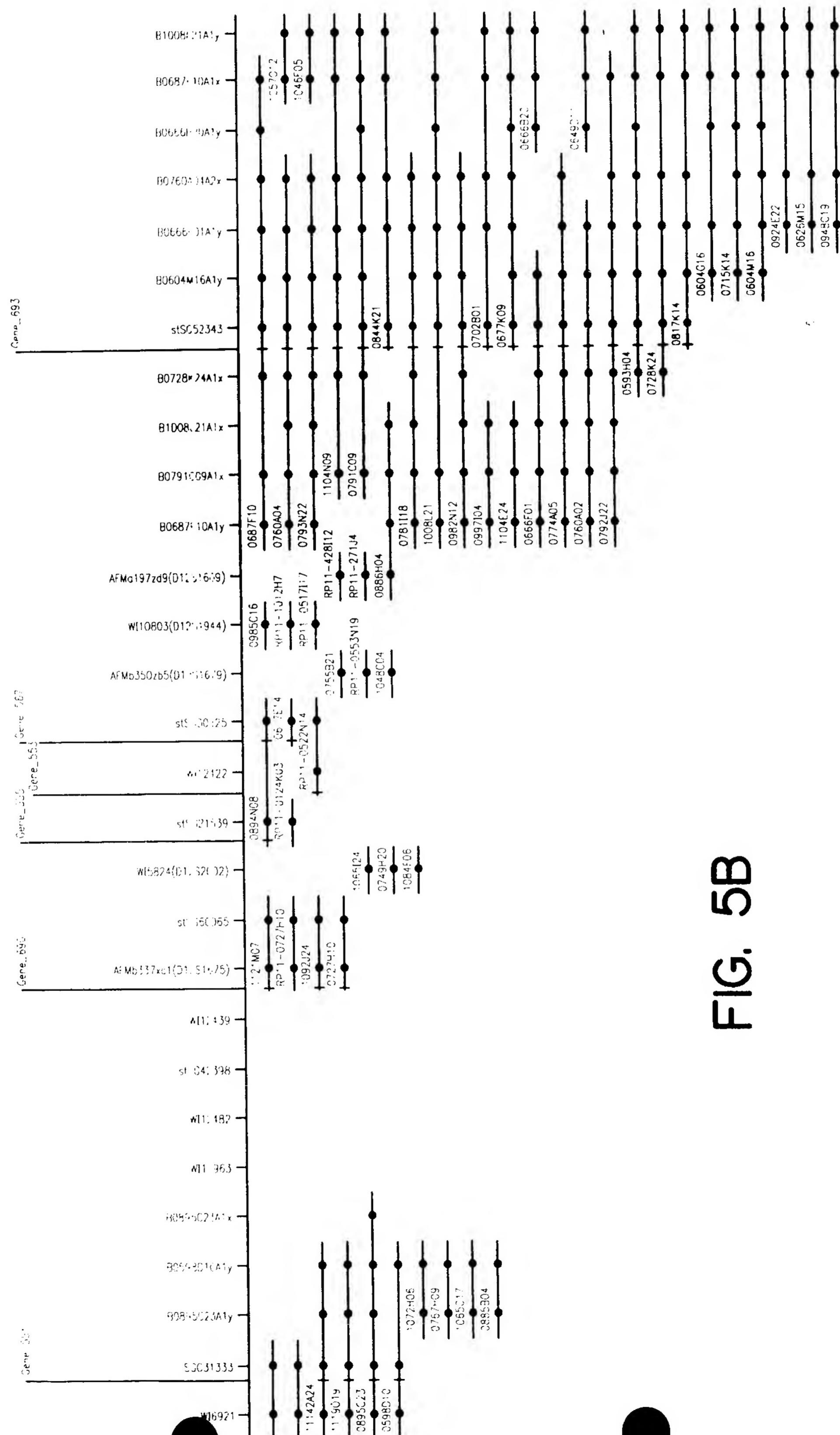


FIG. 4

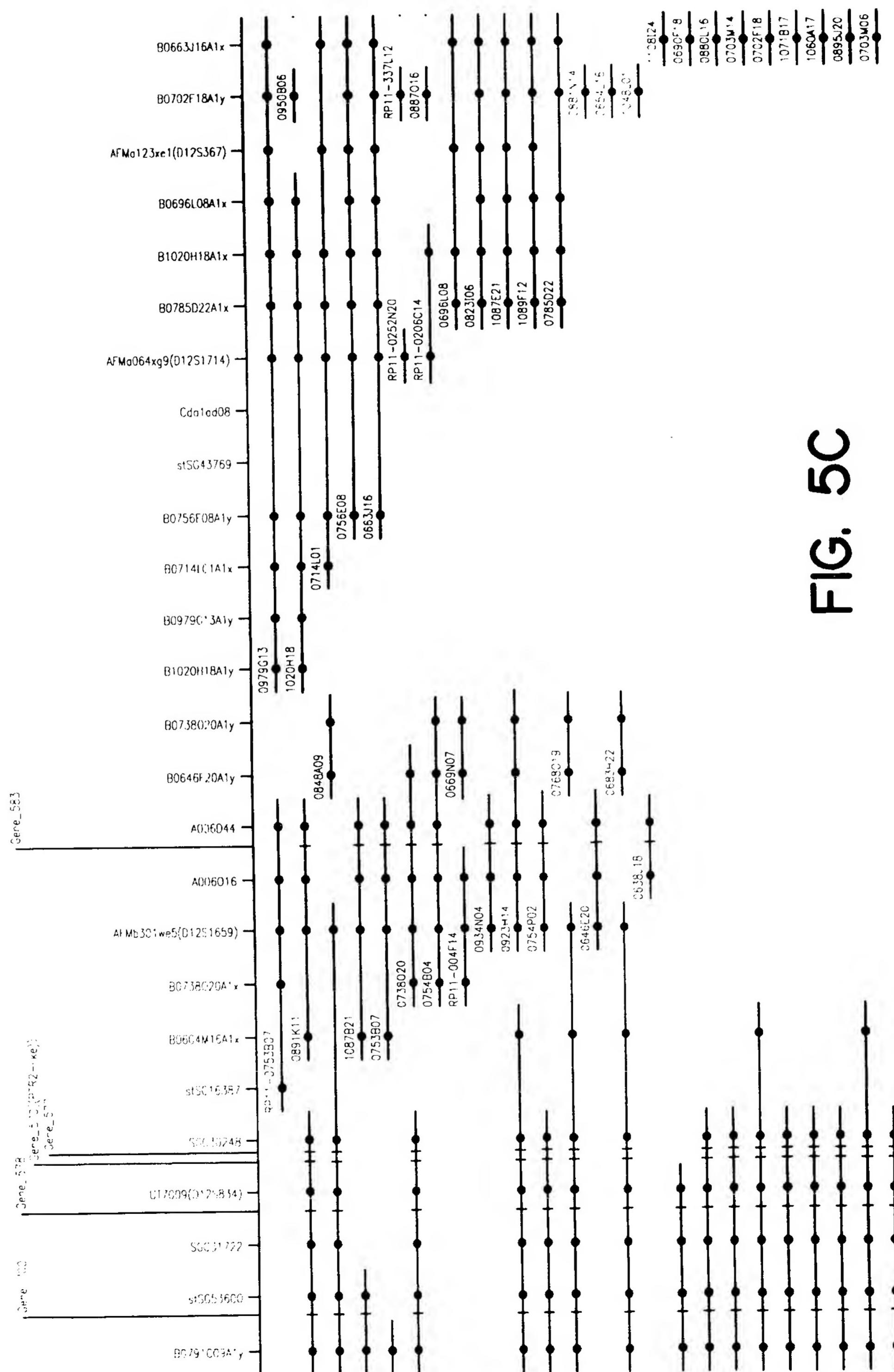
FIG. 5A

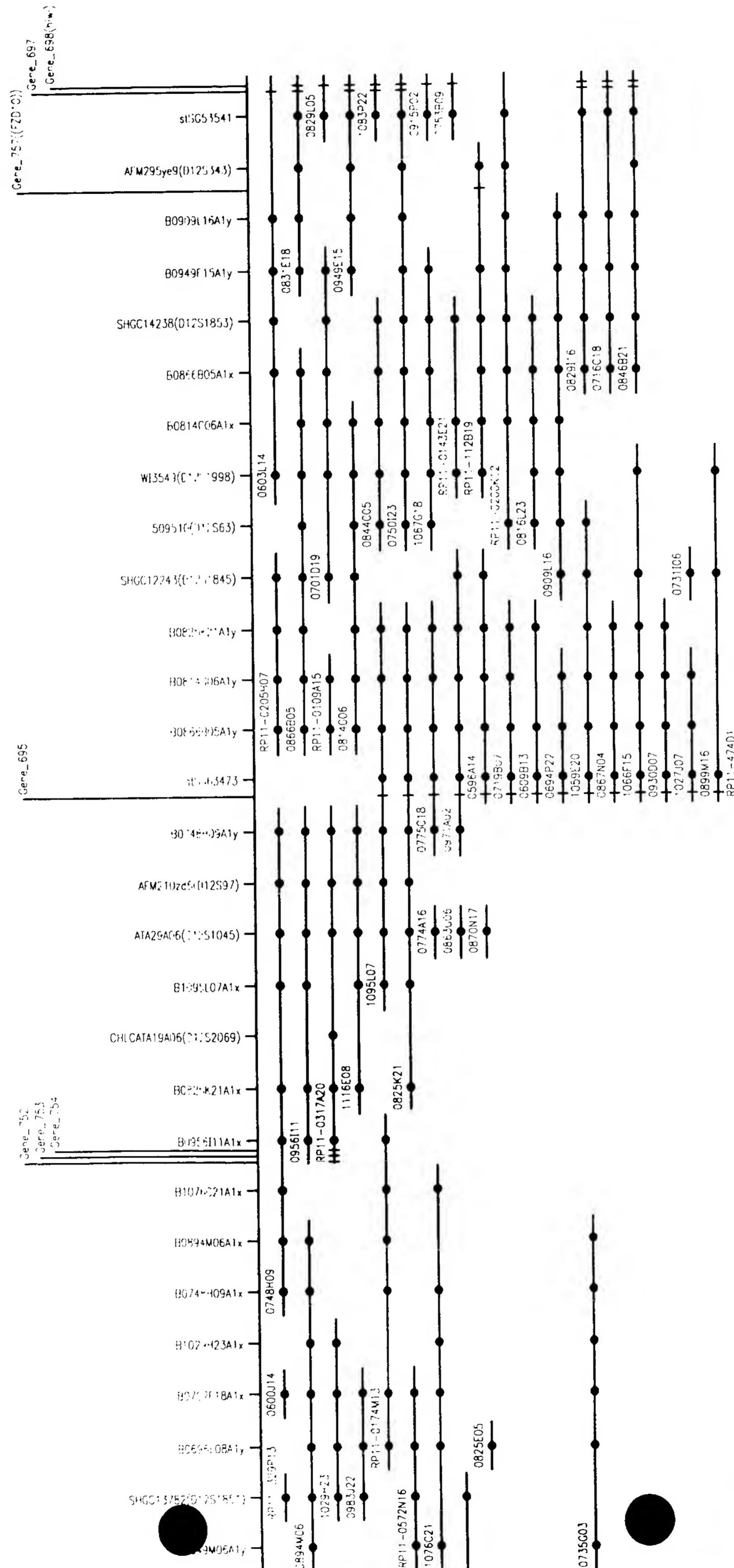




5B
EIGHT

FIG. 5C





5D
FIG.

FIG. 5E

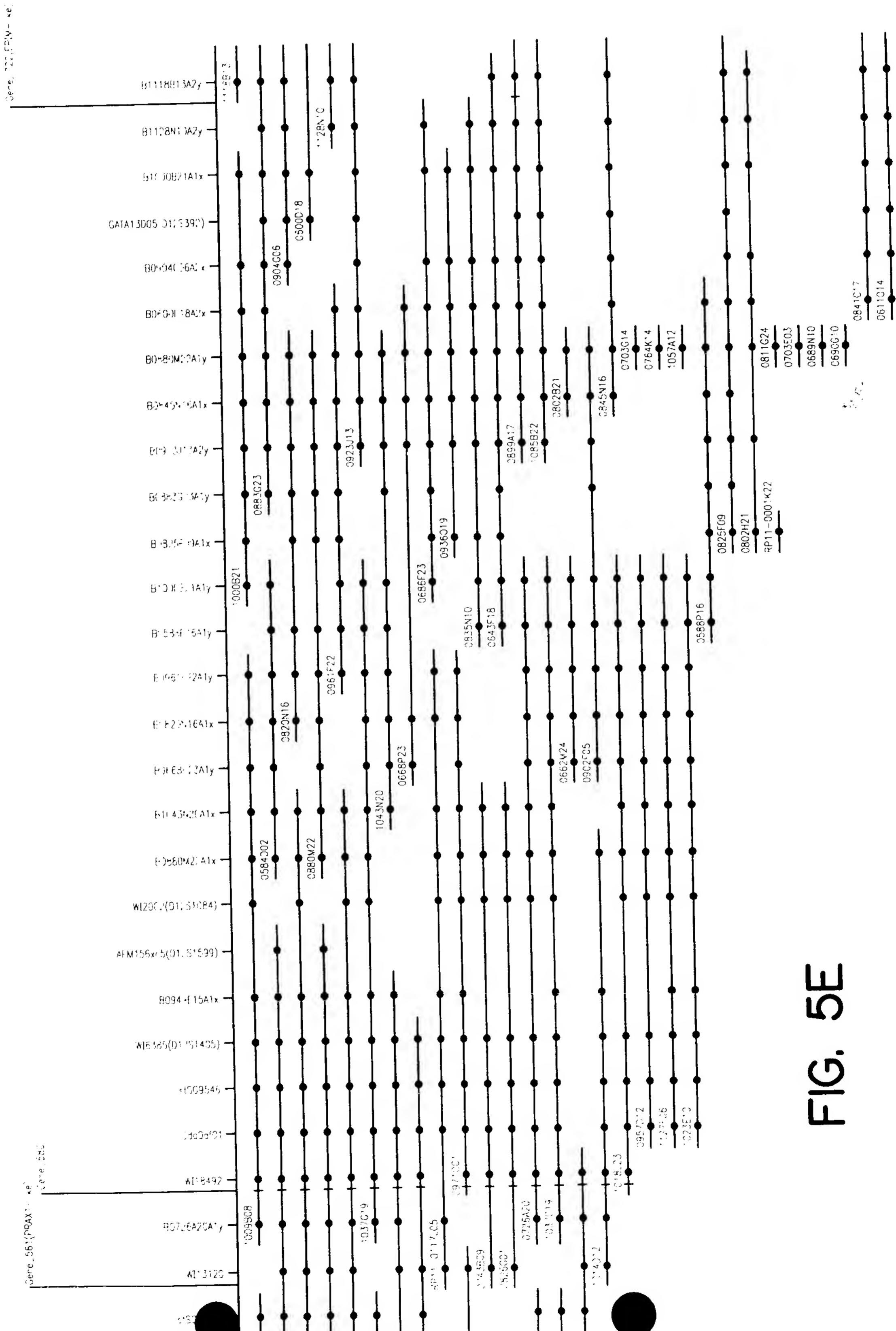


FIG. 5F

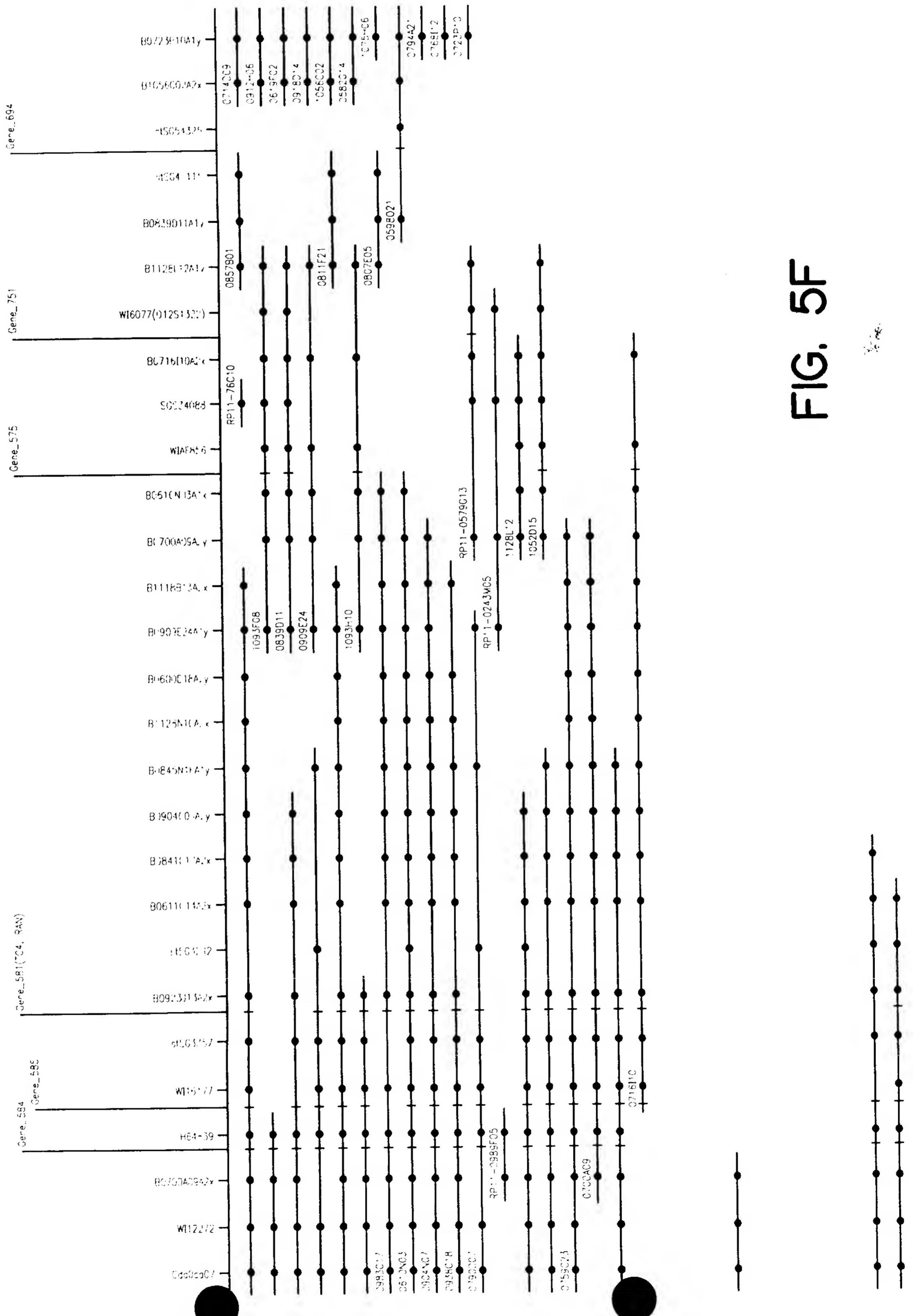


FIG. 5G

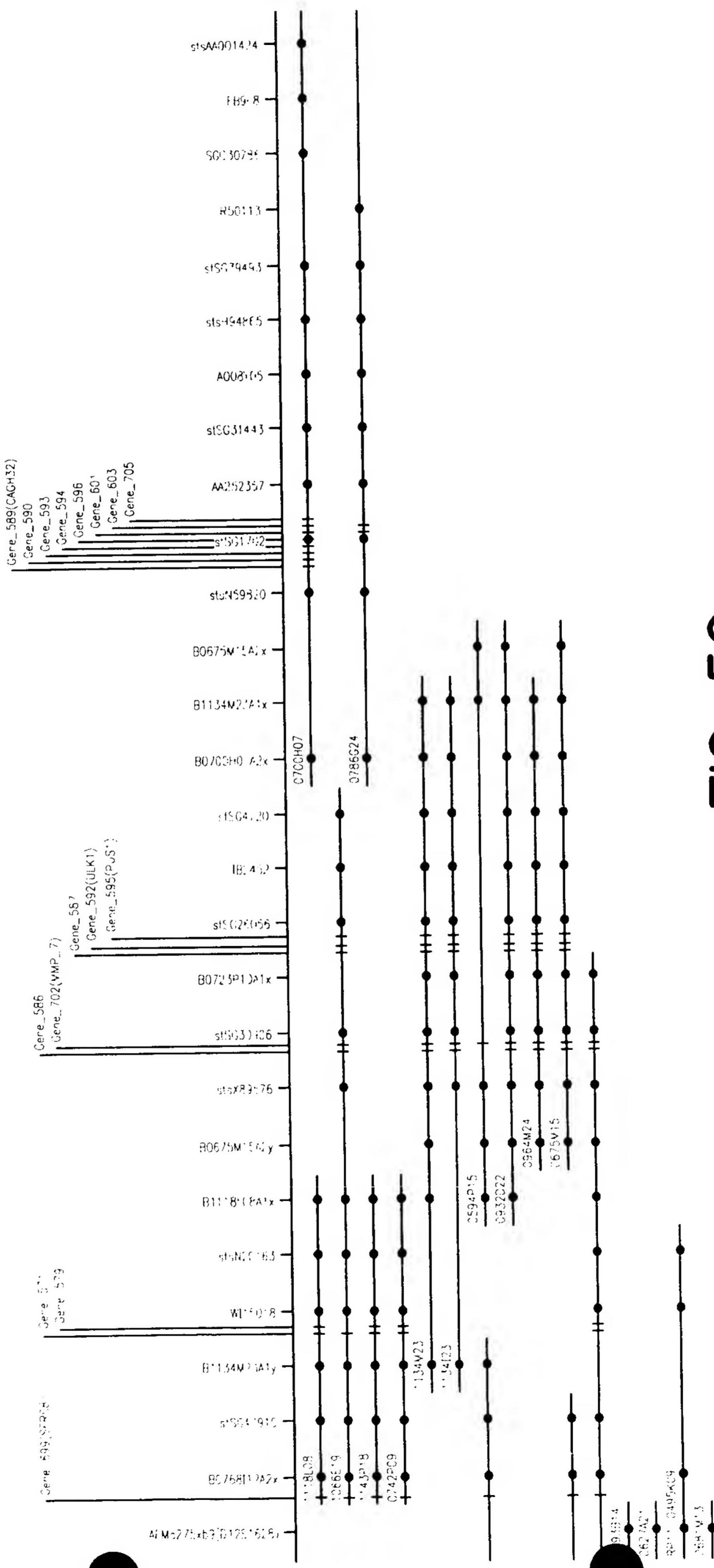
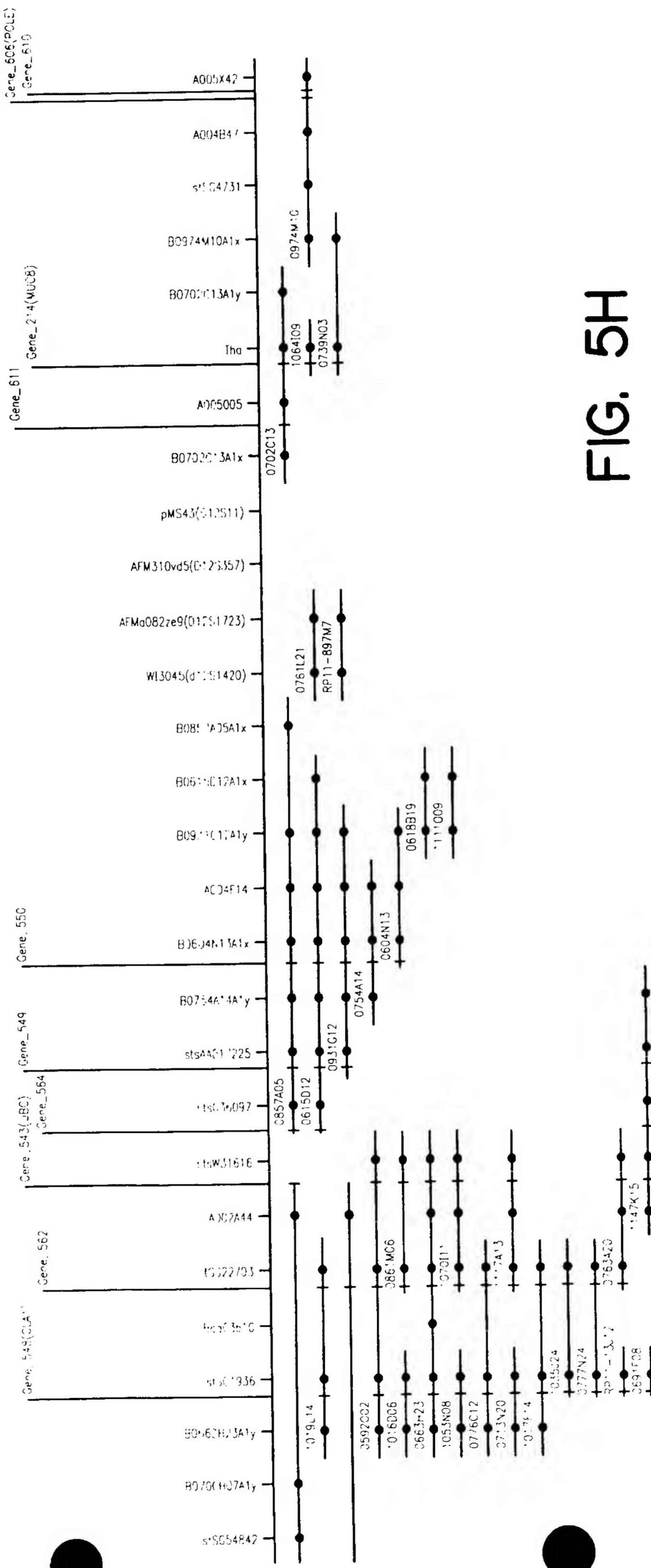
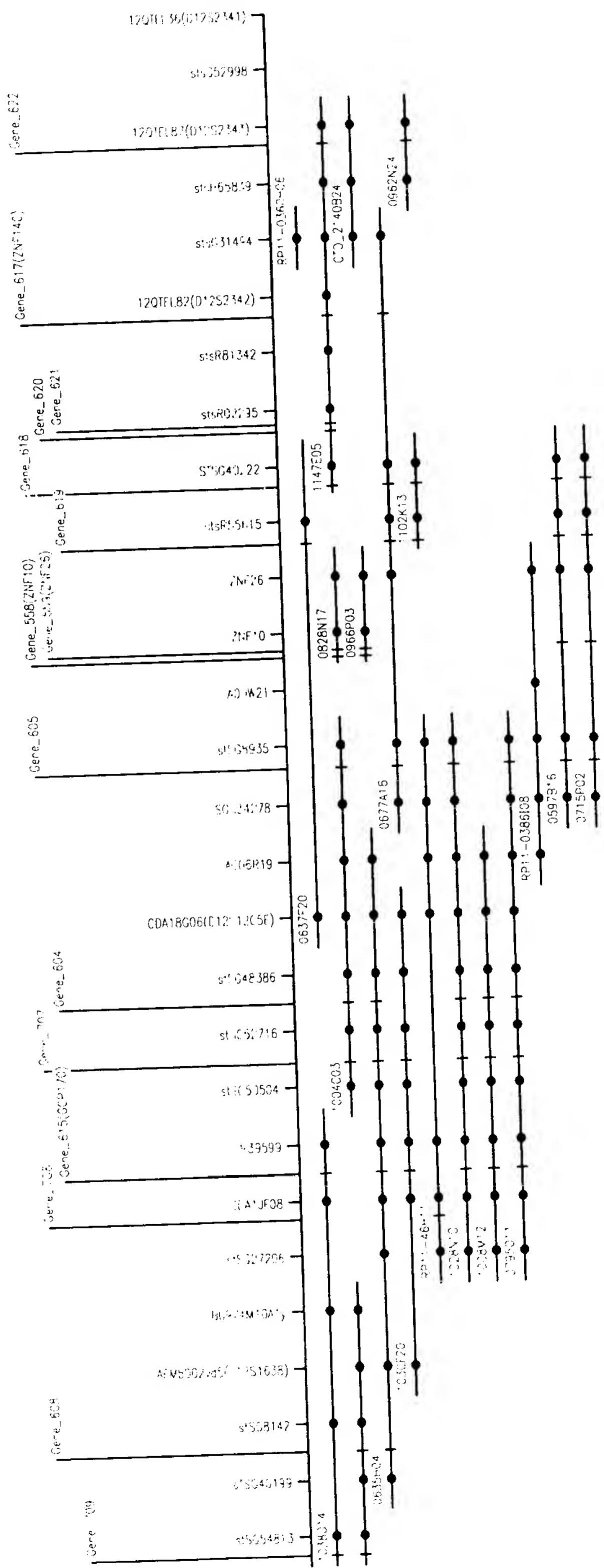


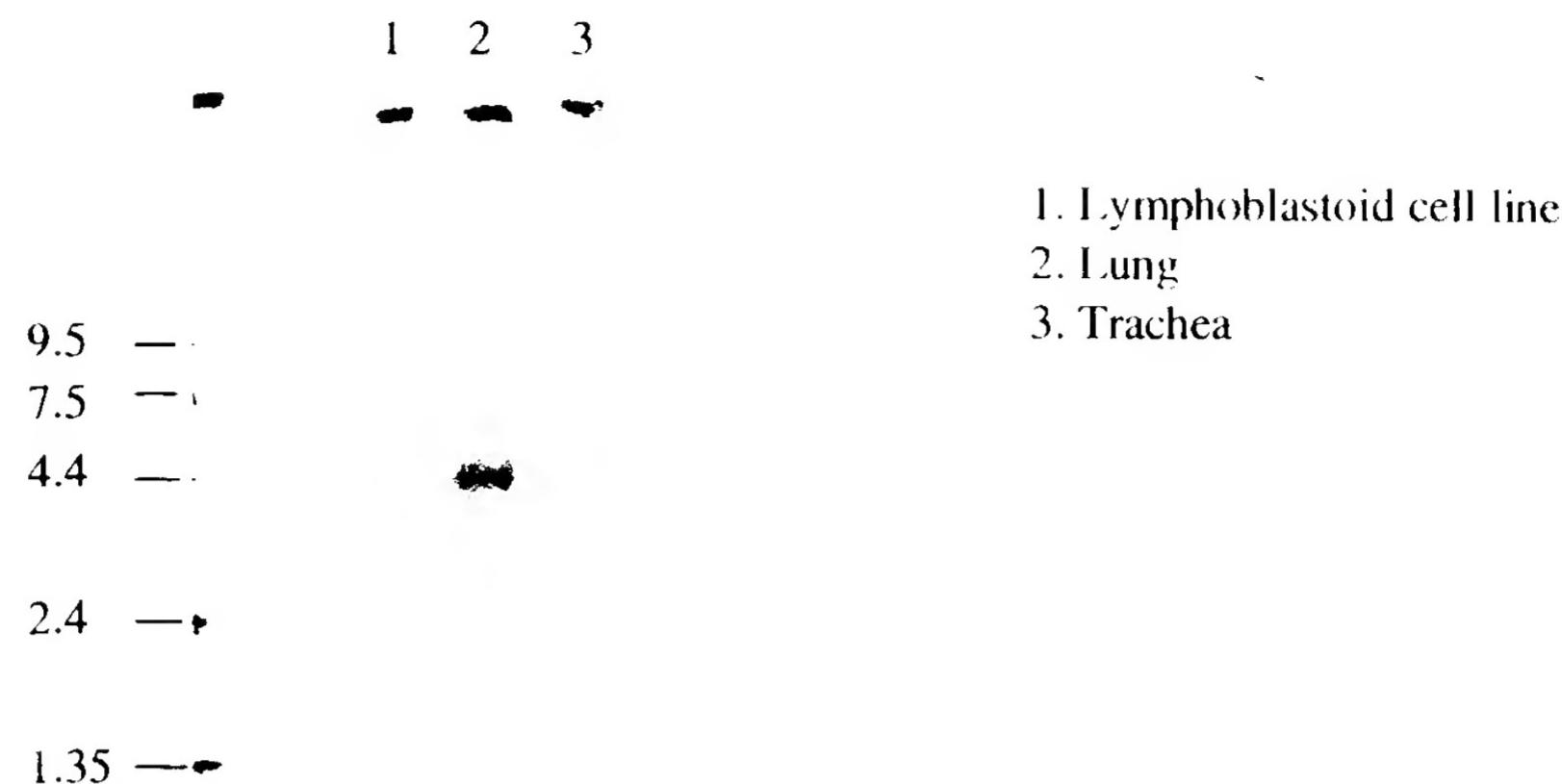
FIG. 5H





FIGURE

Gene 214



Gene 436

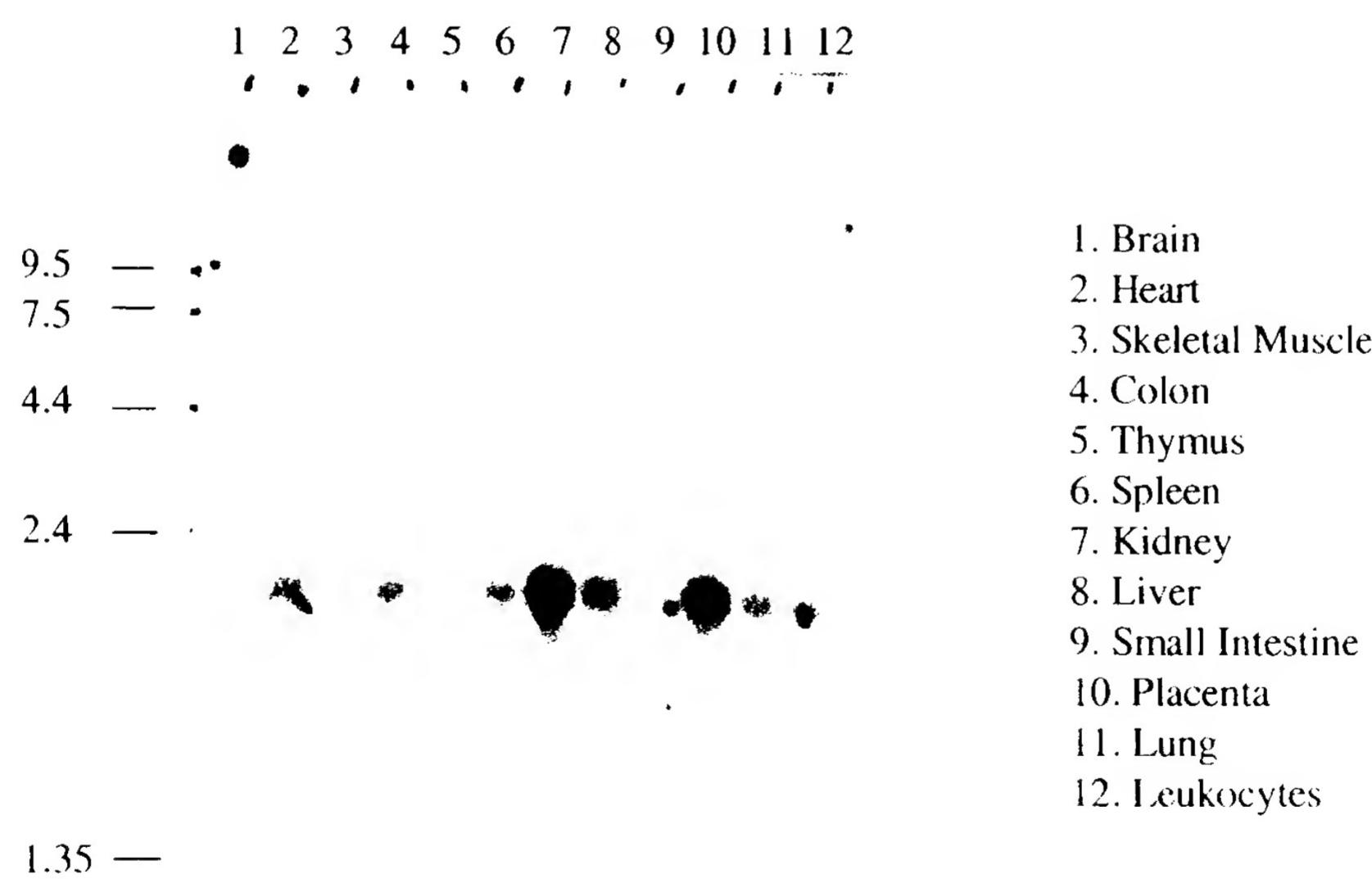
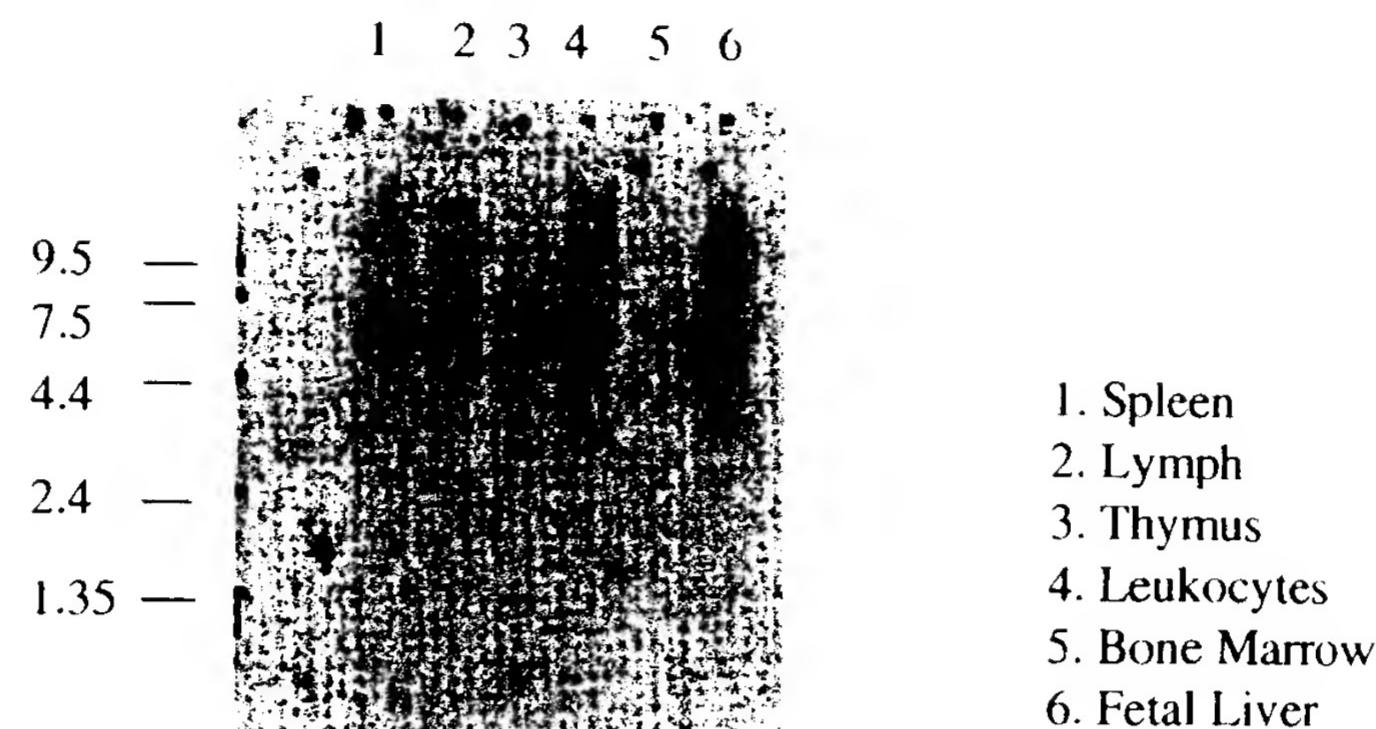


FIG. 6A

Gene 454



Gene 515

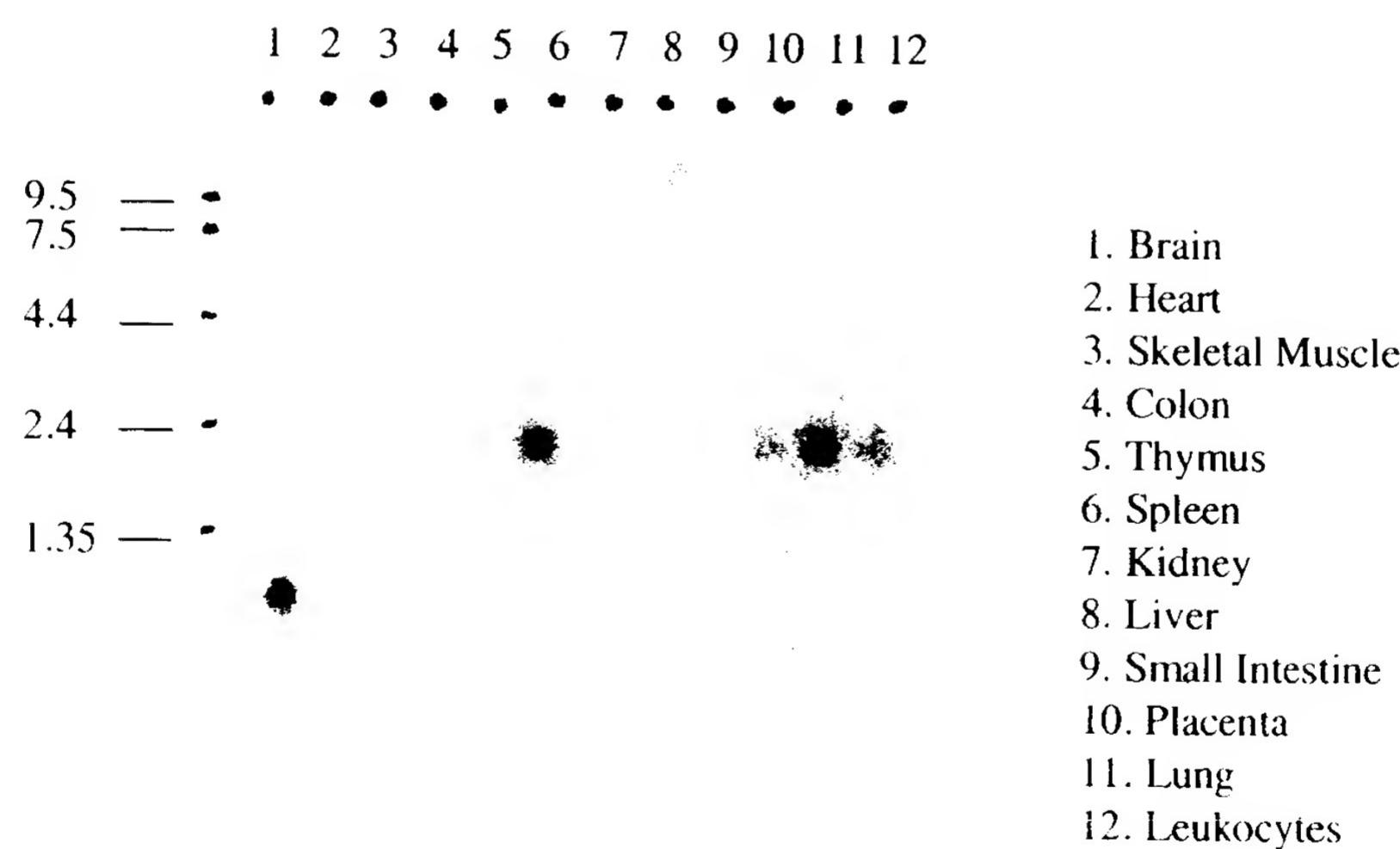
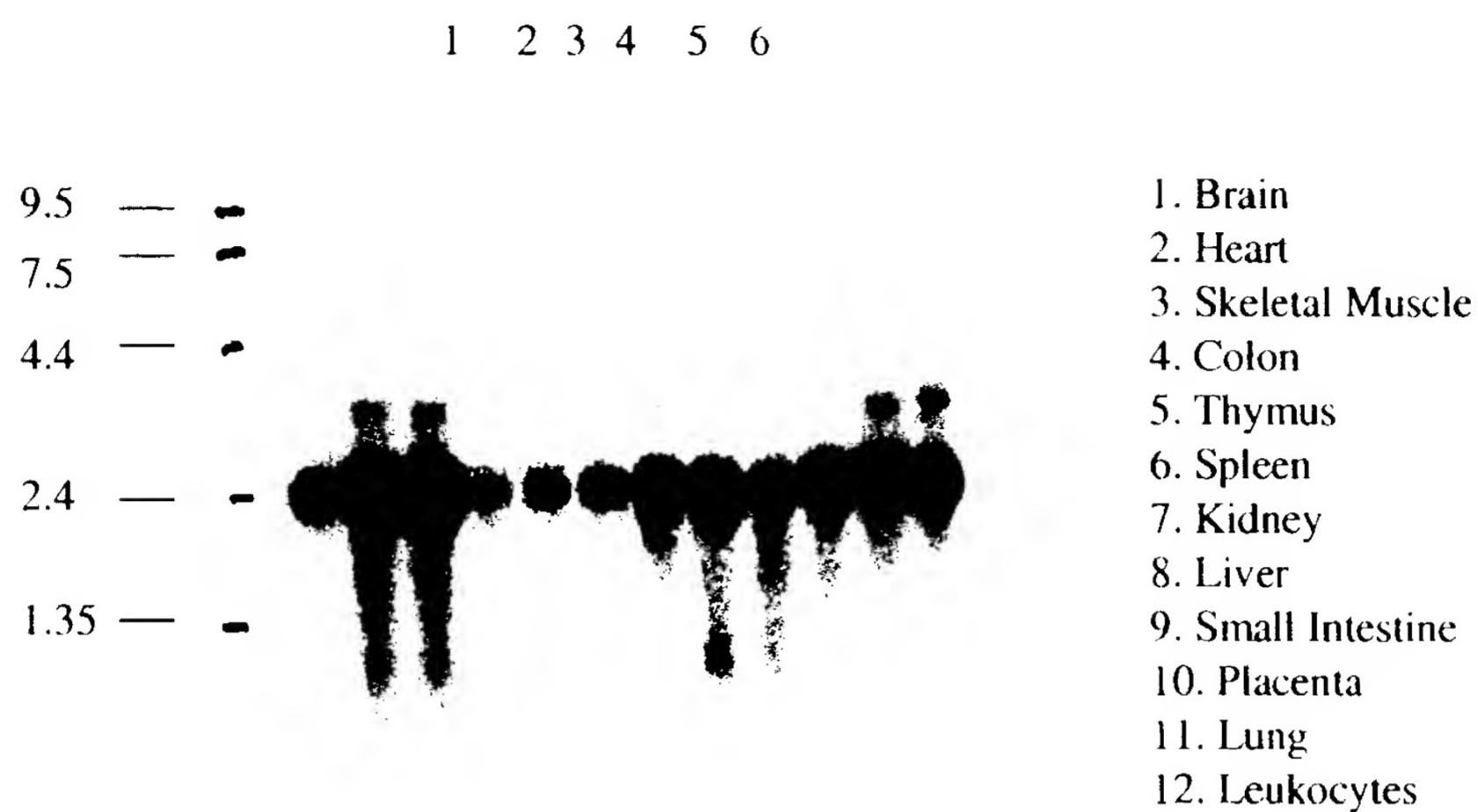


FIG. 6B

Gene 543

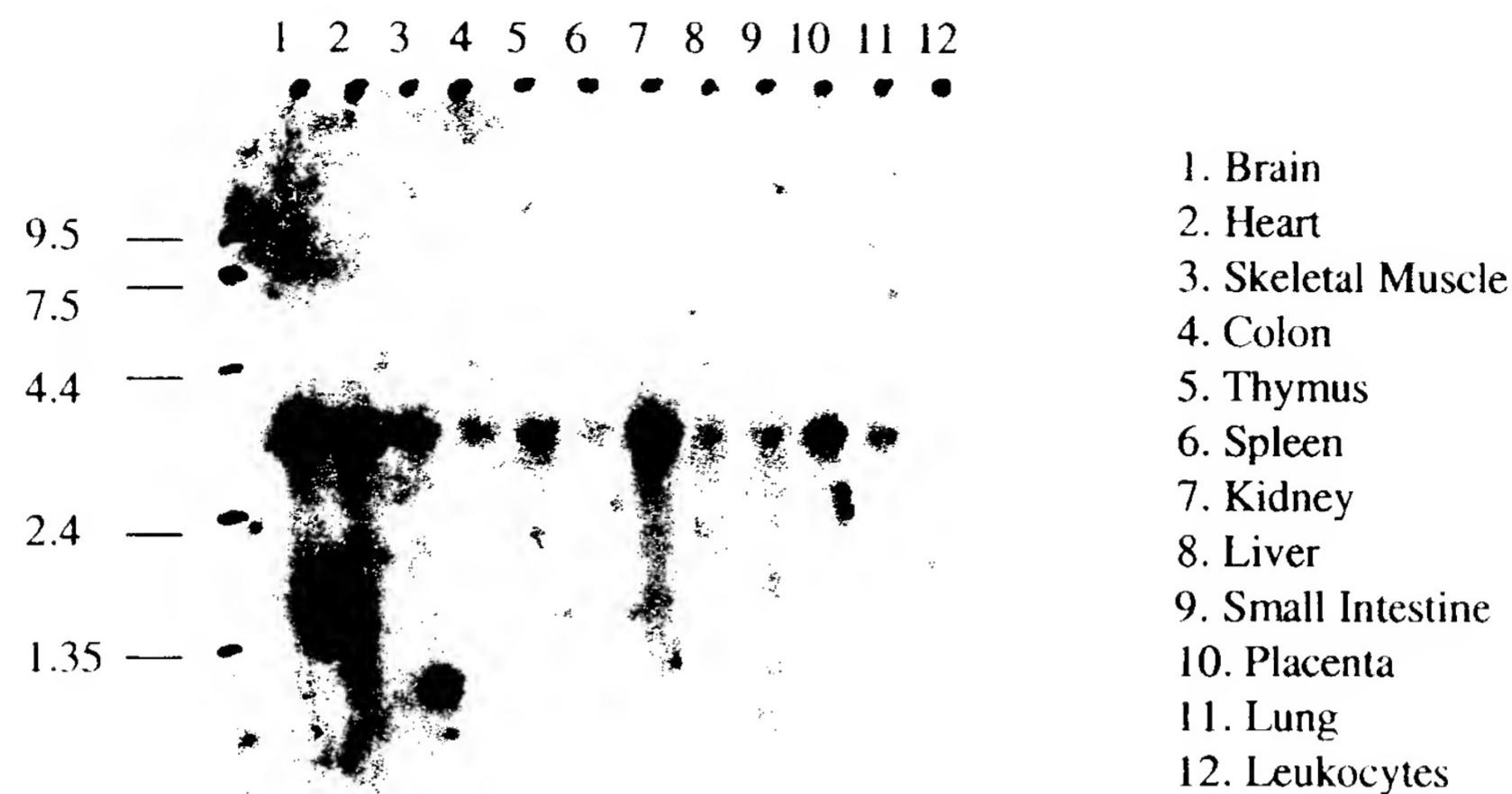


Gene 548



FIG. 6C

Gene 550



Gene 561

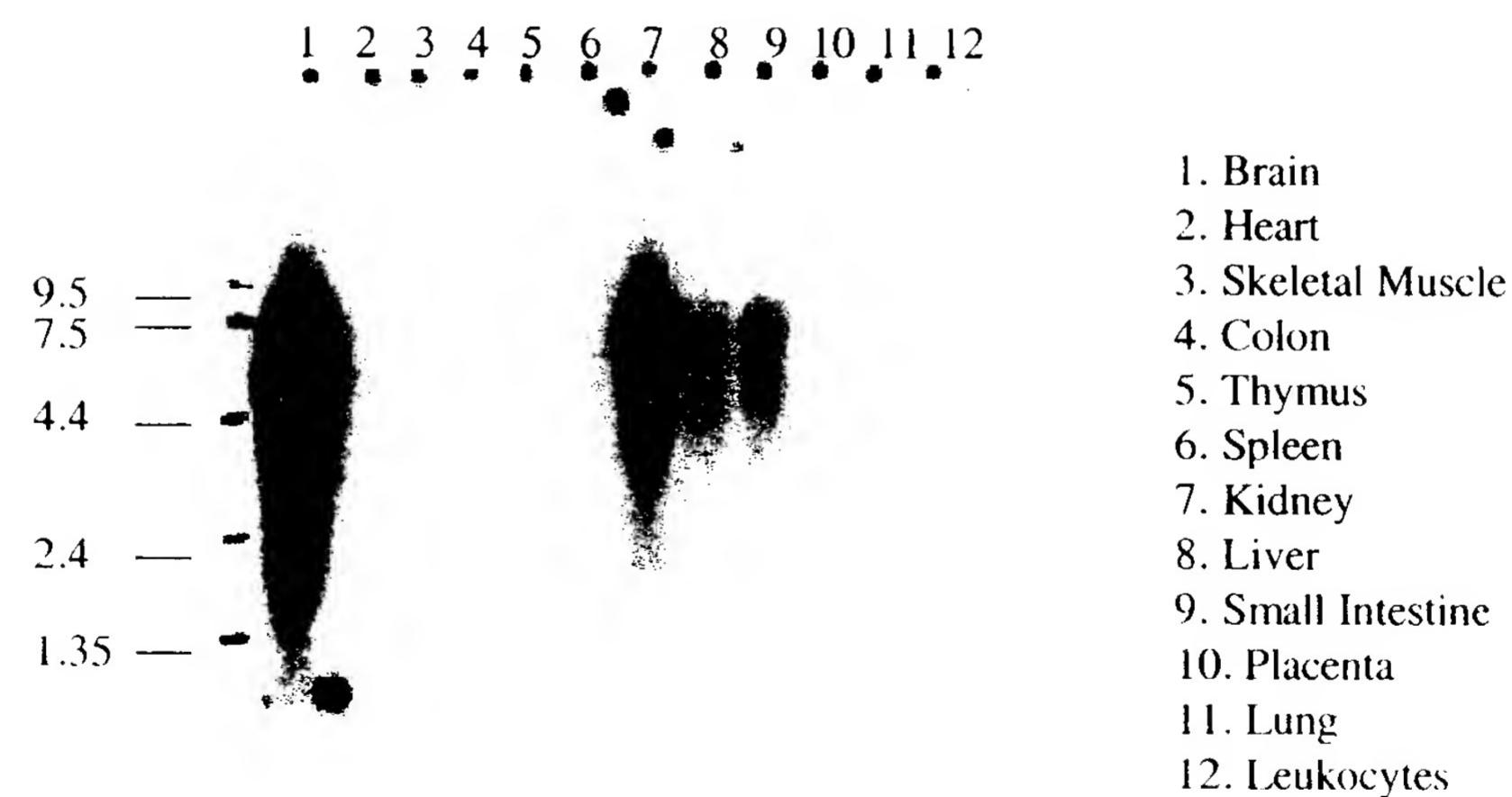
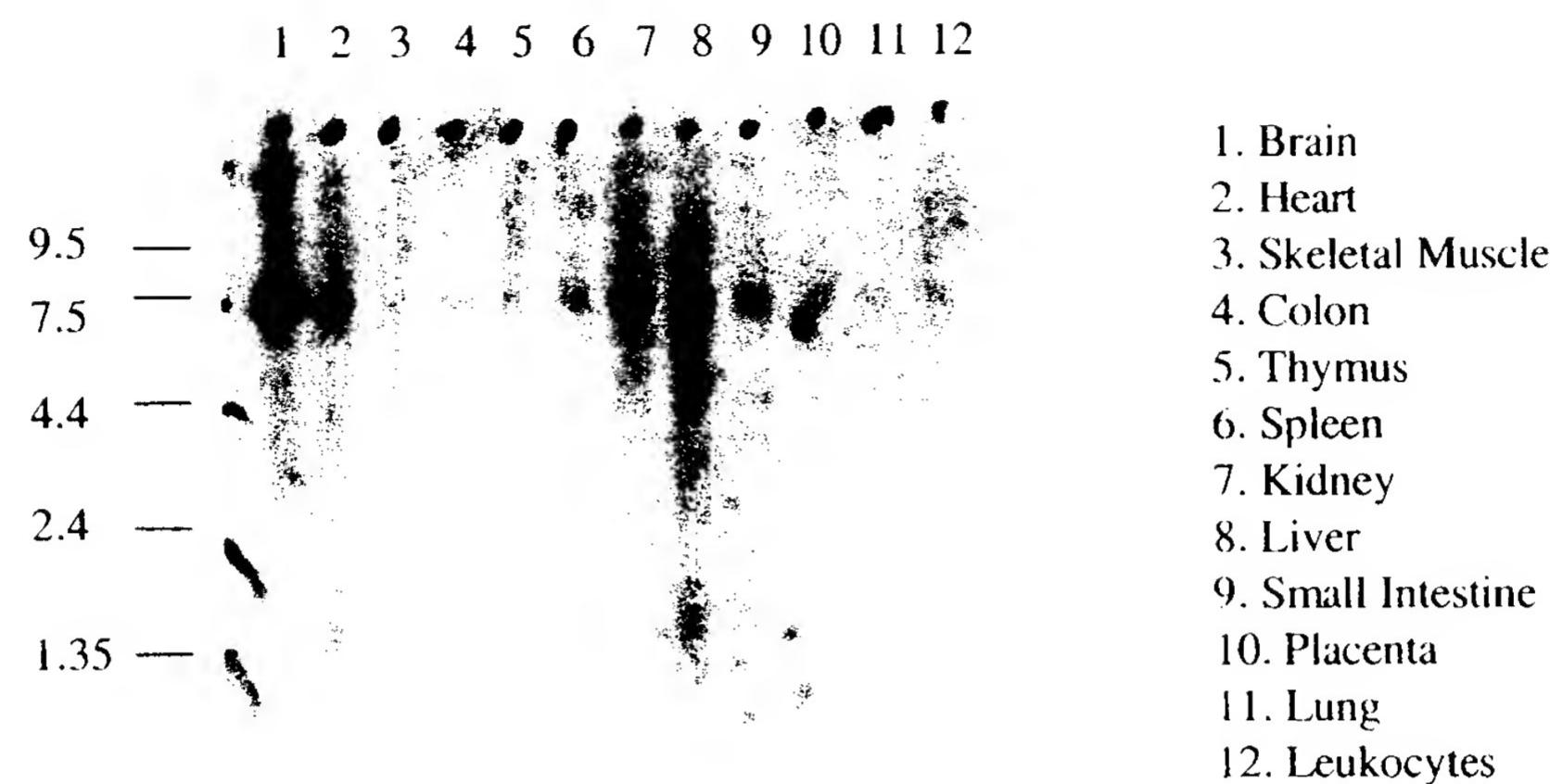


FIG. 6D

Gene 564



Gene 570

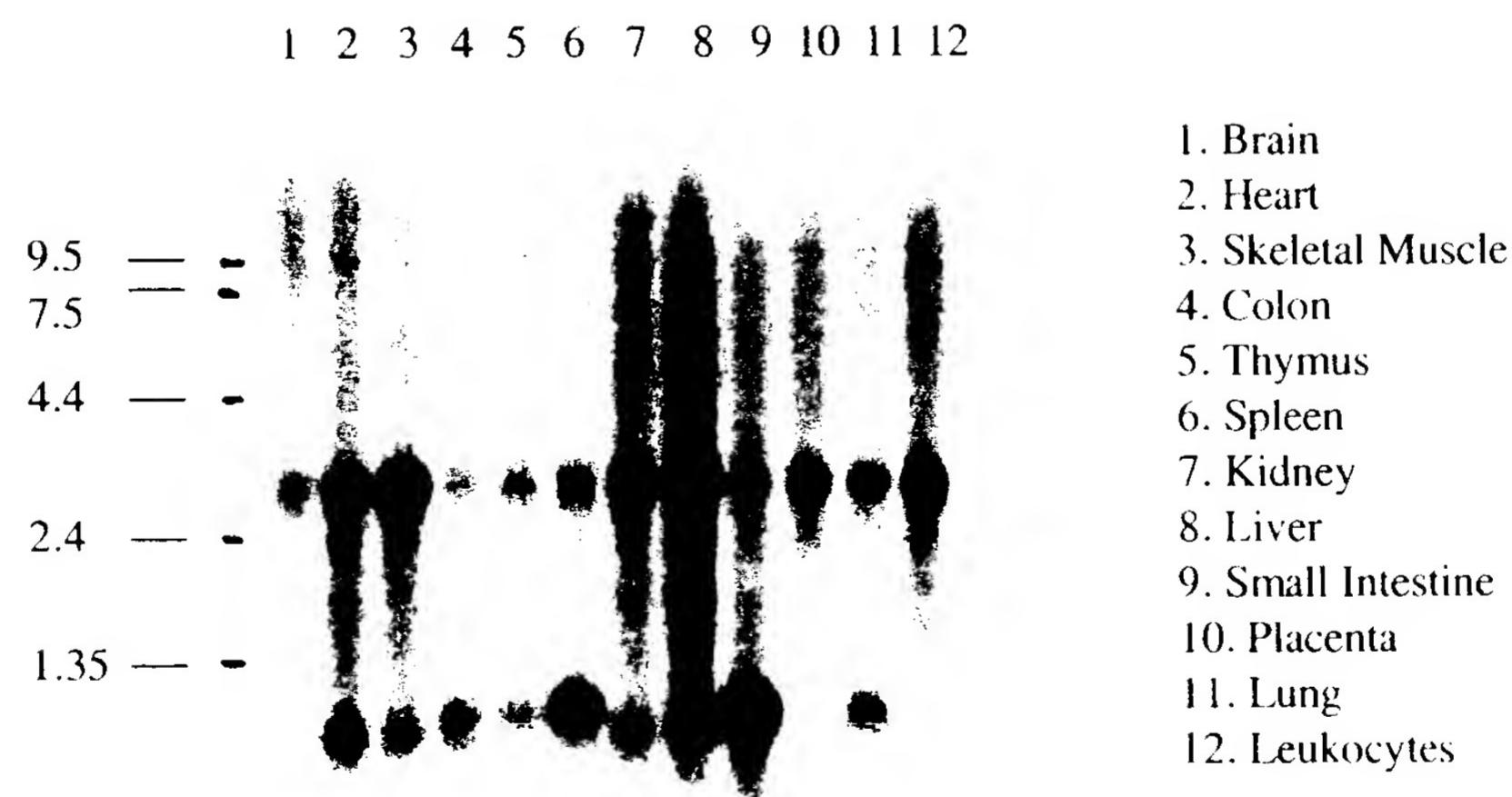
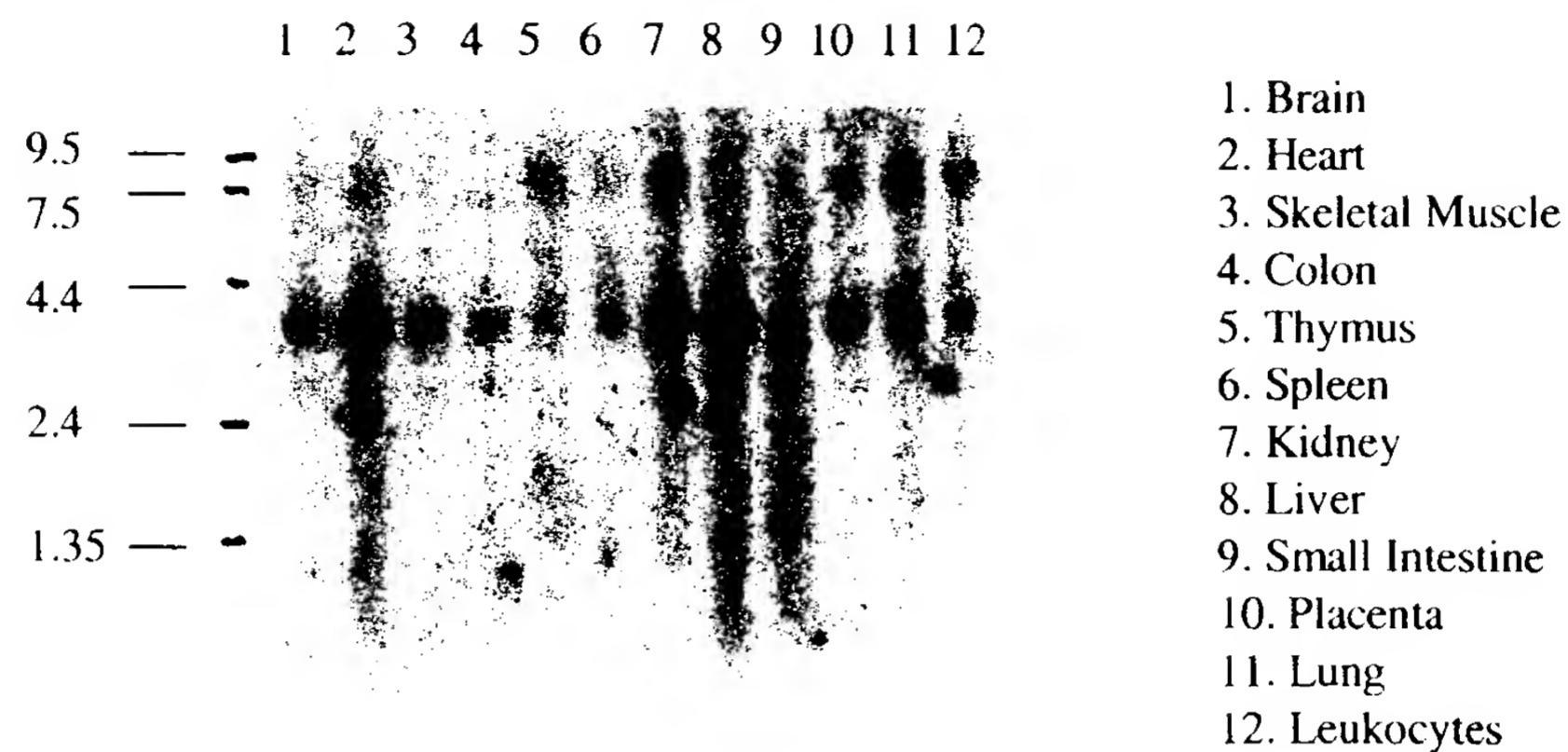


FIG. 6E

Gene 576



Gene 577

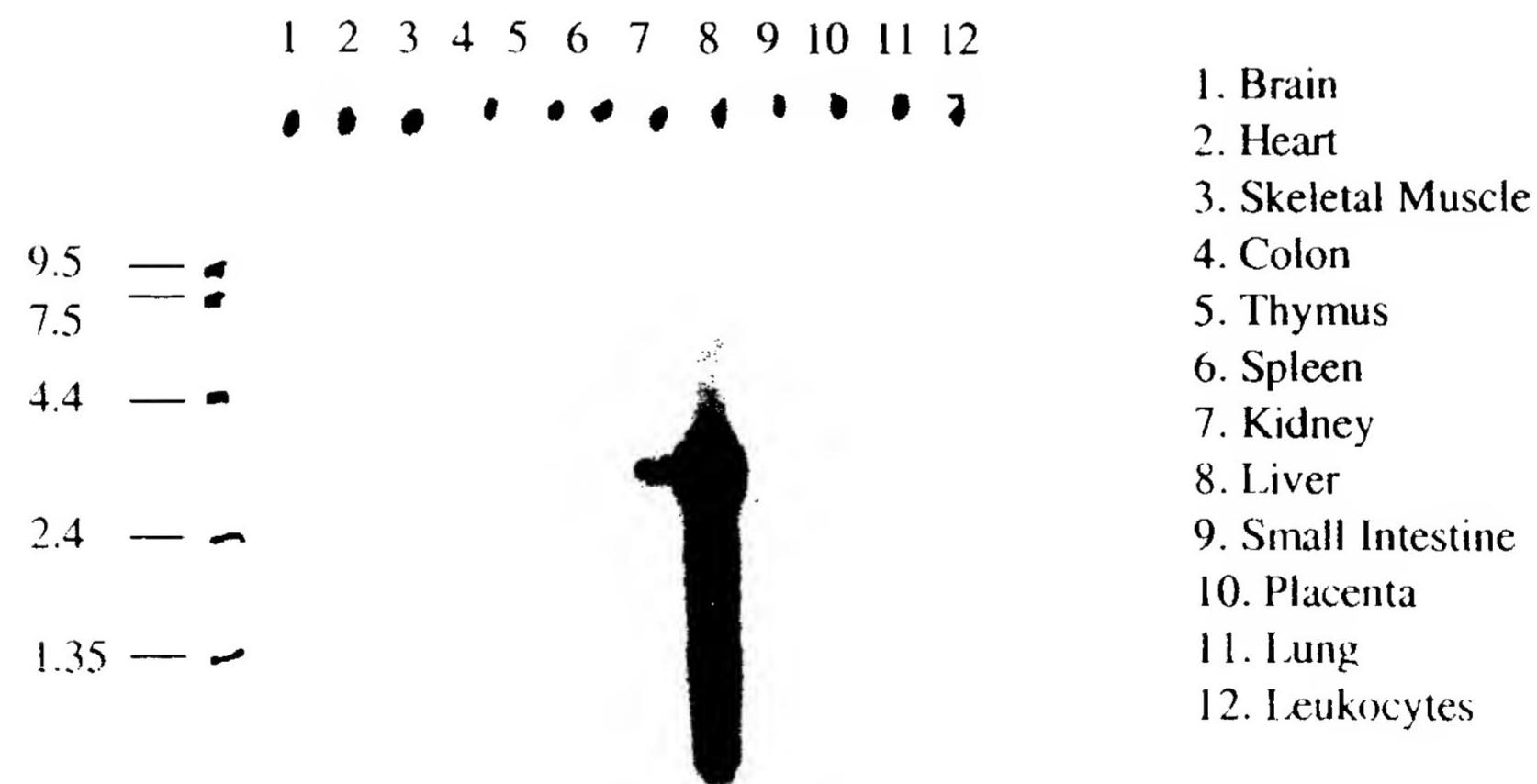
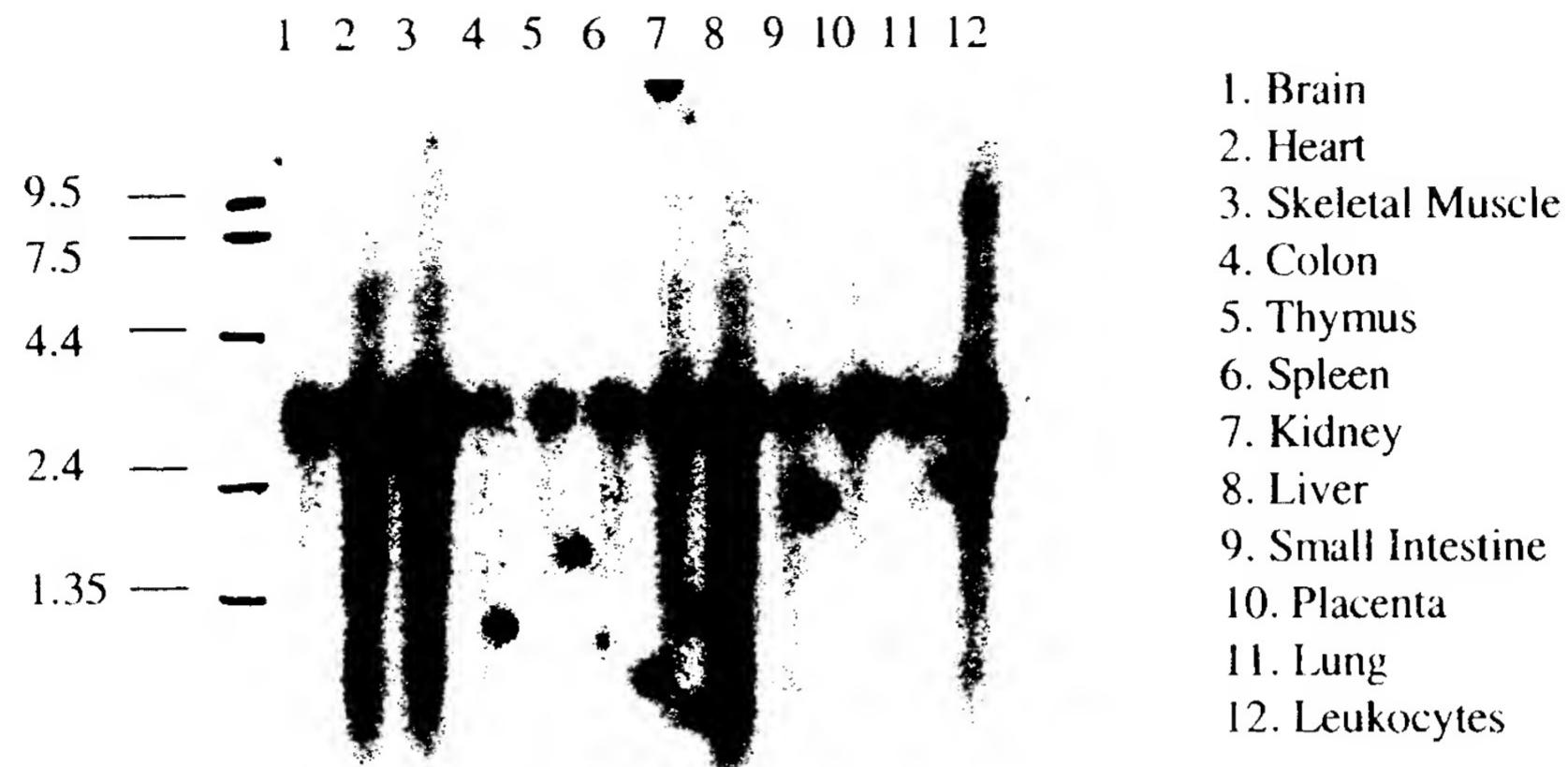


FIG. 6F

Gene 578



Gene 579

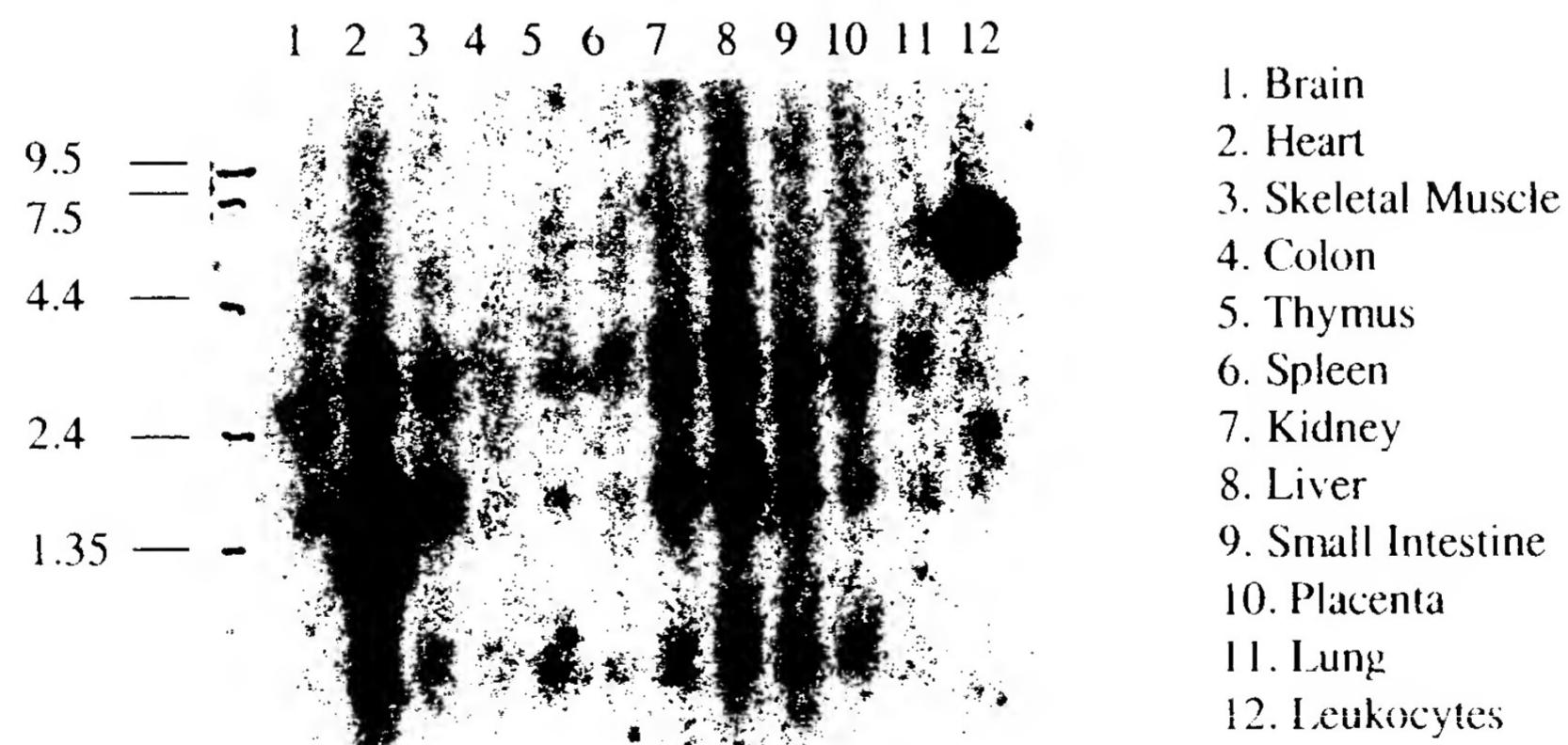


FIG. 6G

Gene 580



Gene 581

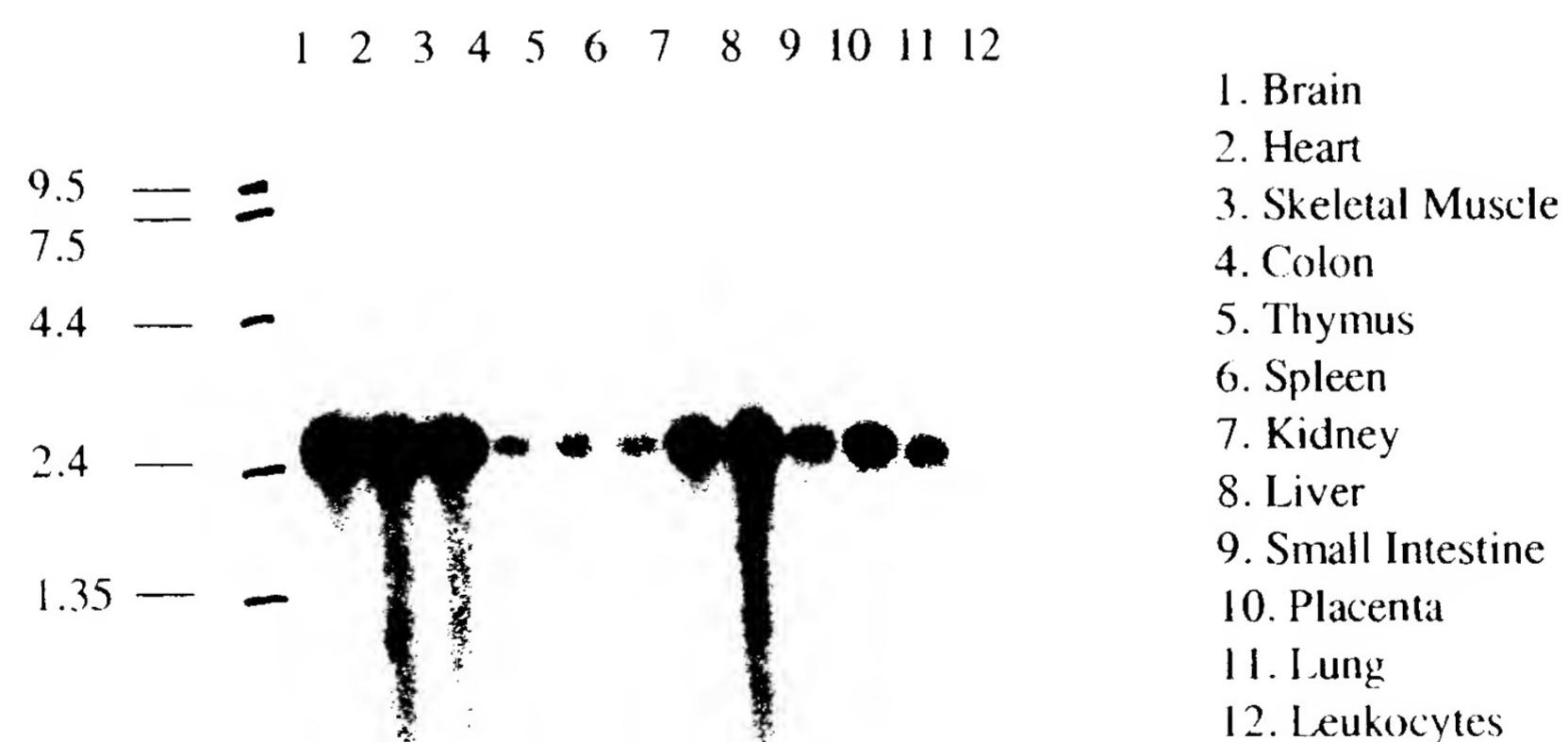
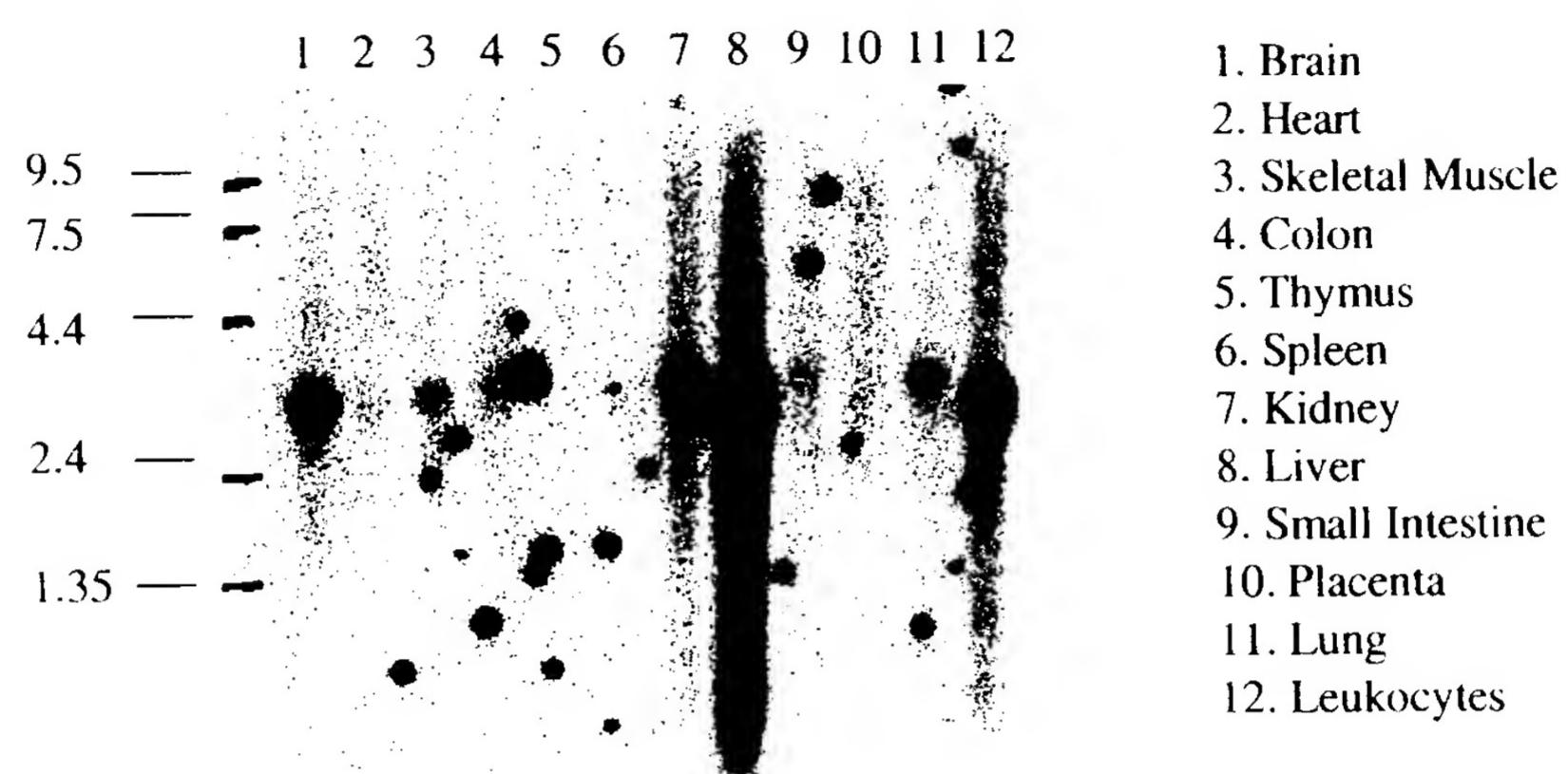


FIG. 6H

Gene 583



Gene 589

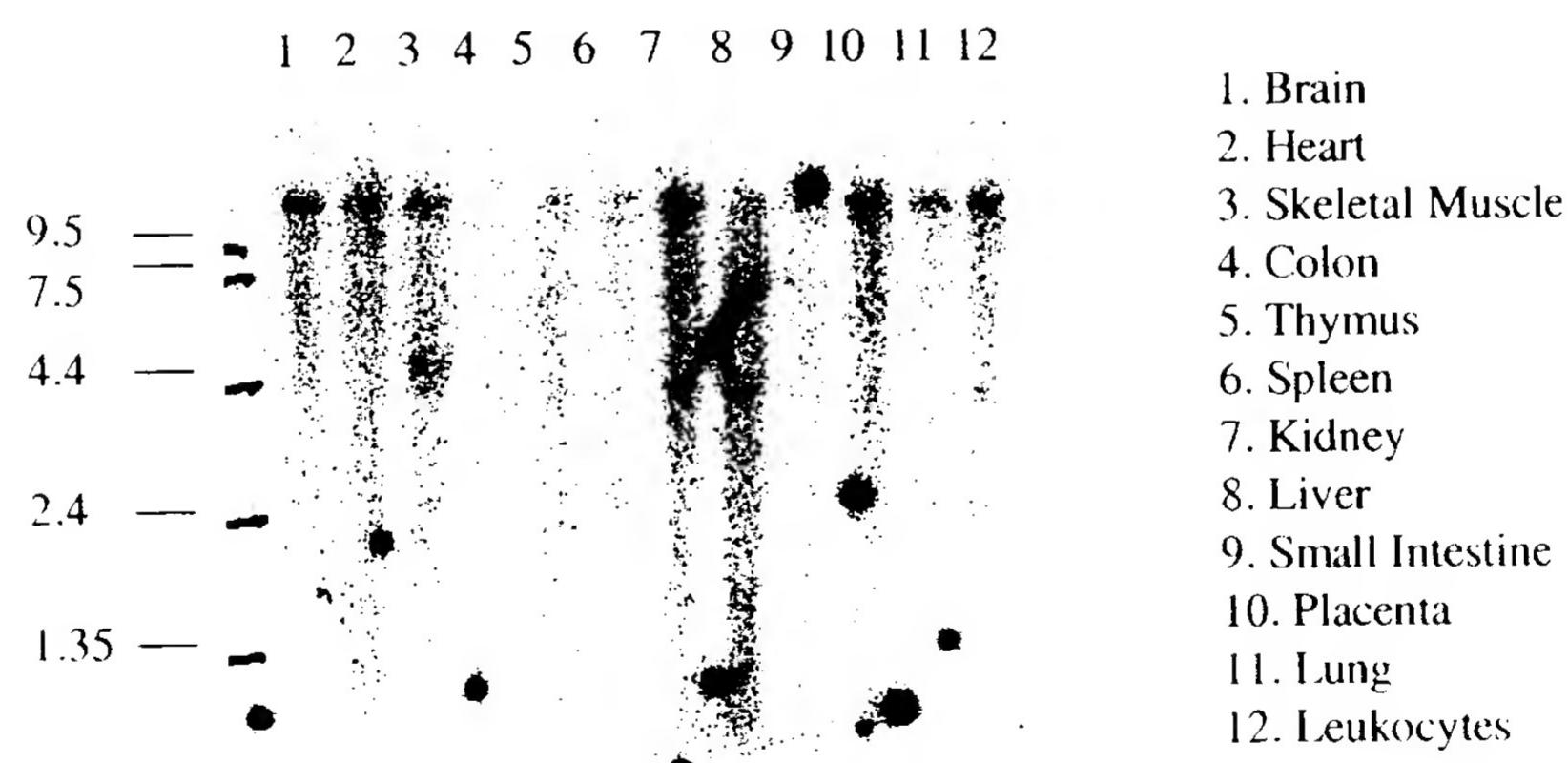
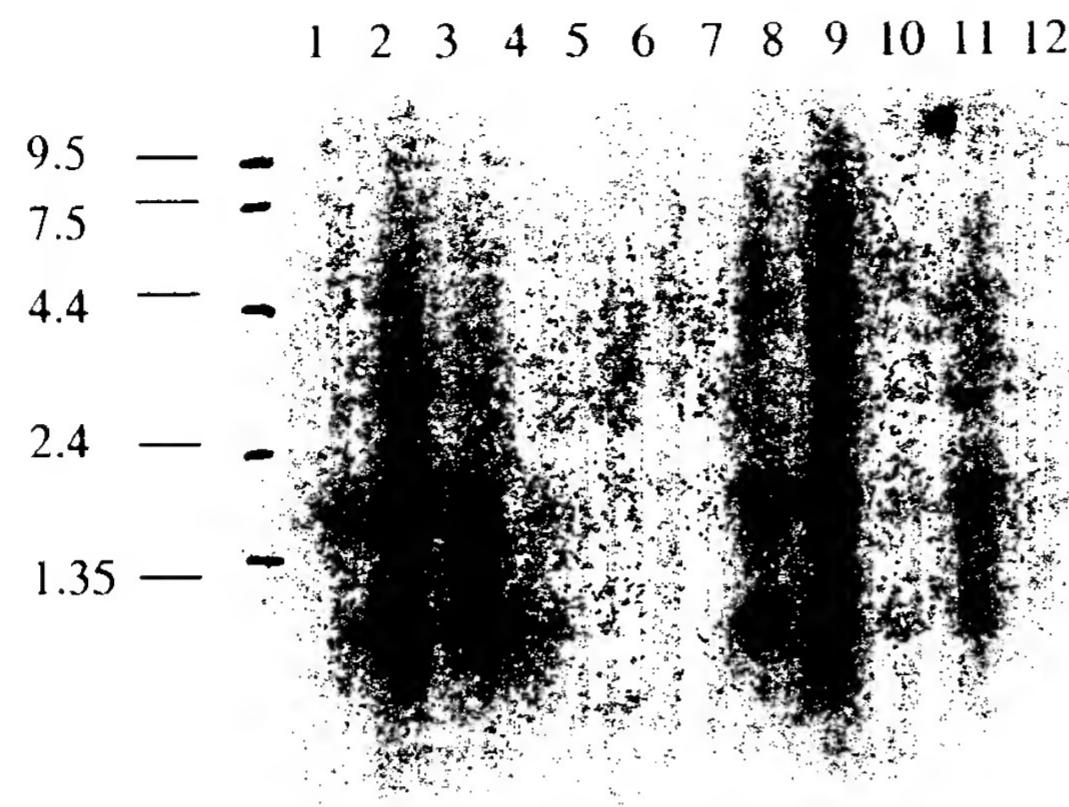


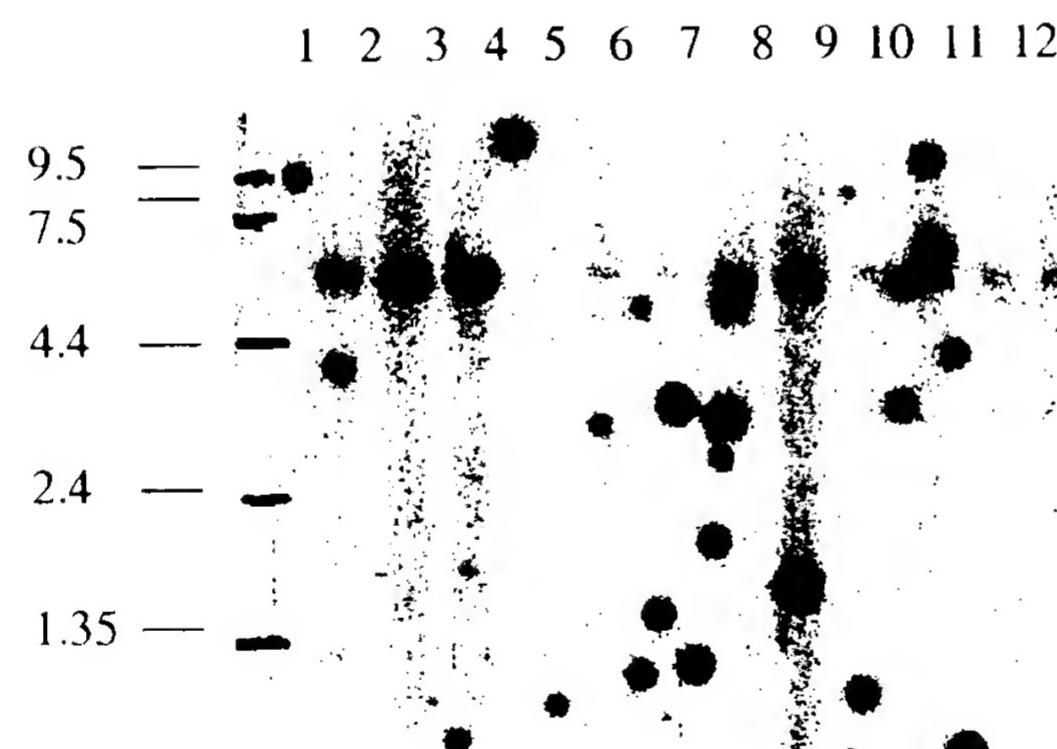
FIG. 6I

Gene 590



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

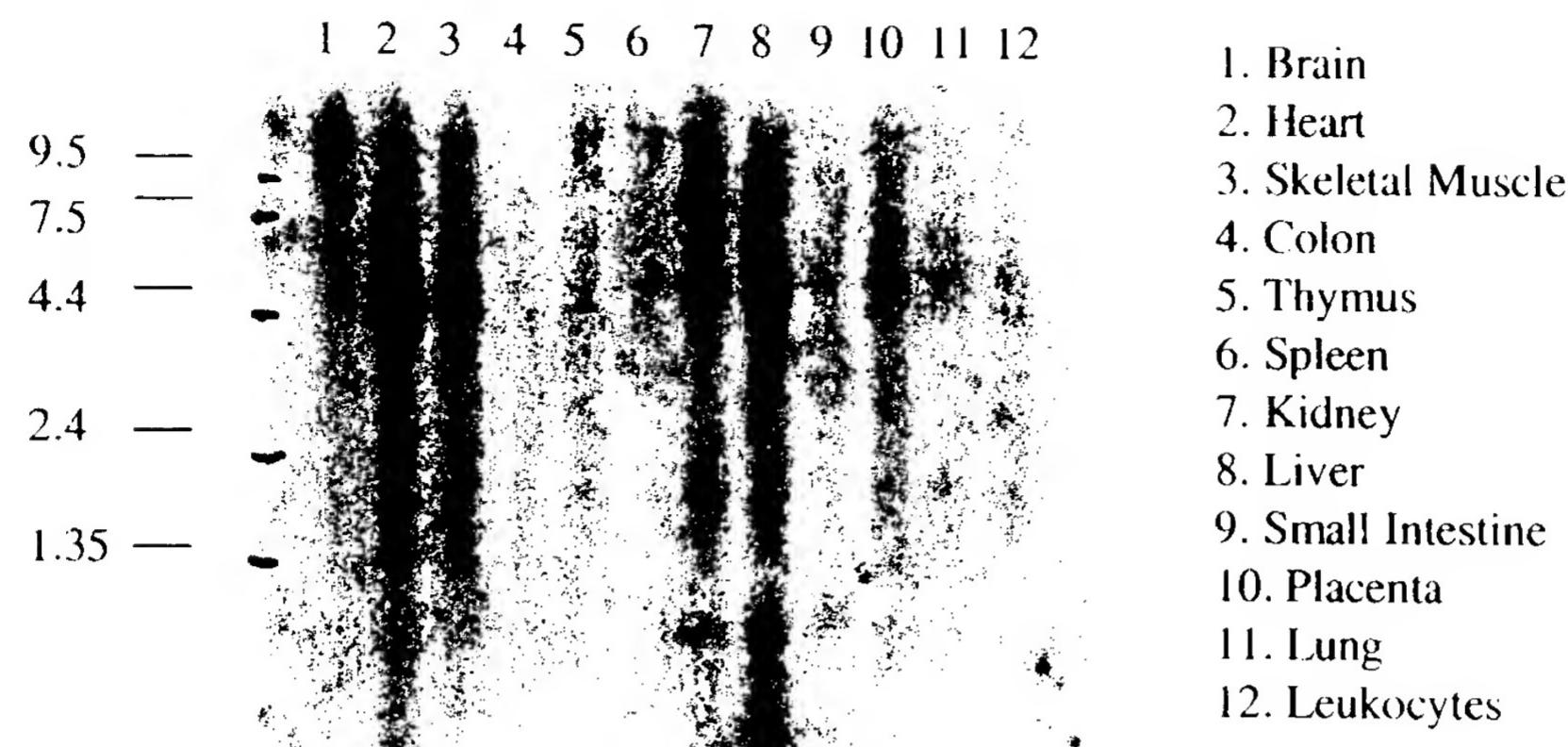
Gene 592



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6J

Gene 594

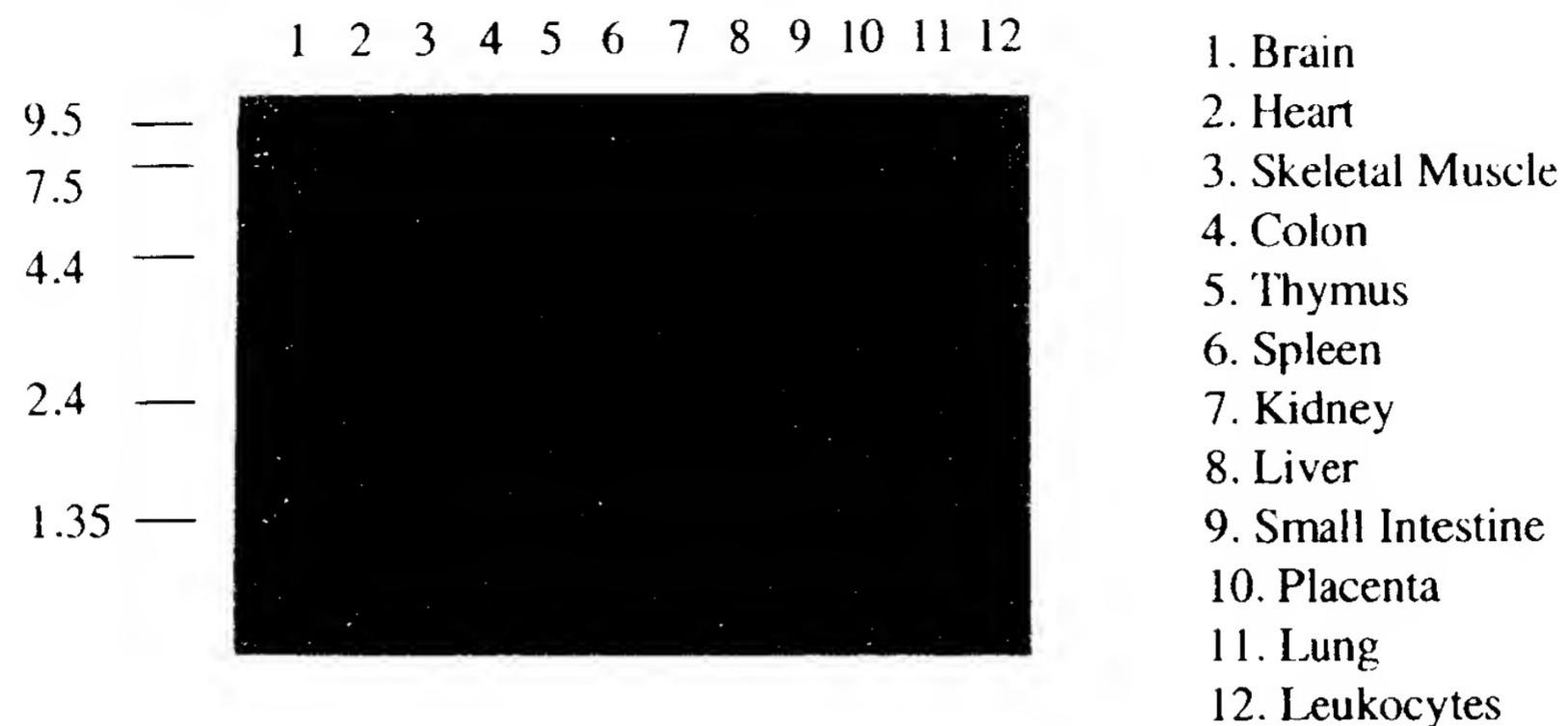


Gene 595



FIG. 6K

Gene 596



Gene 604

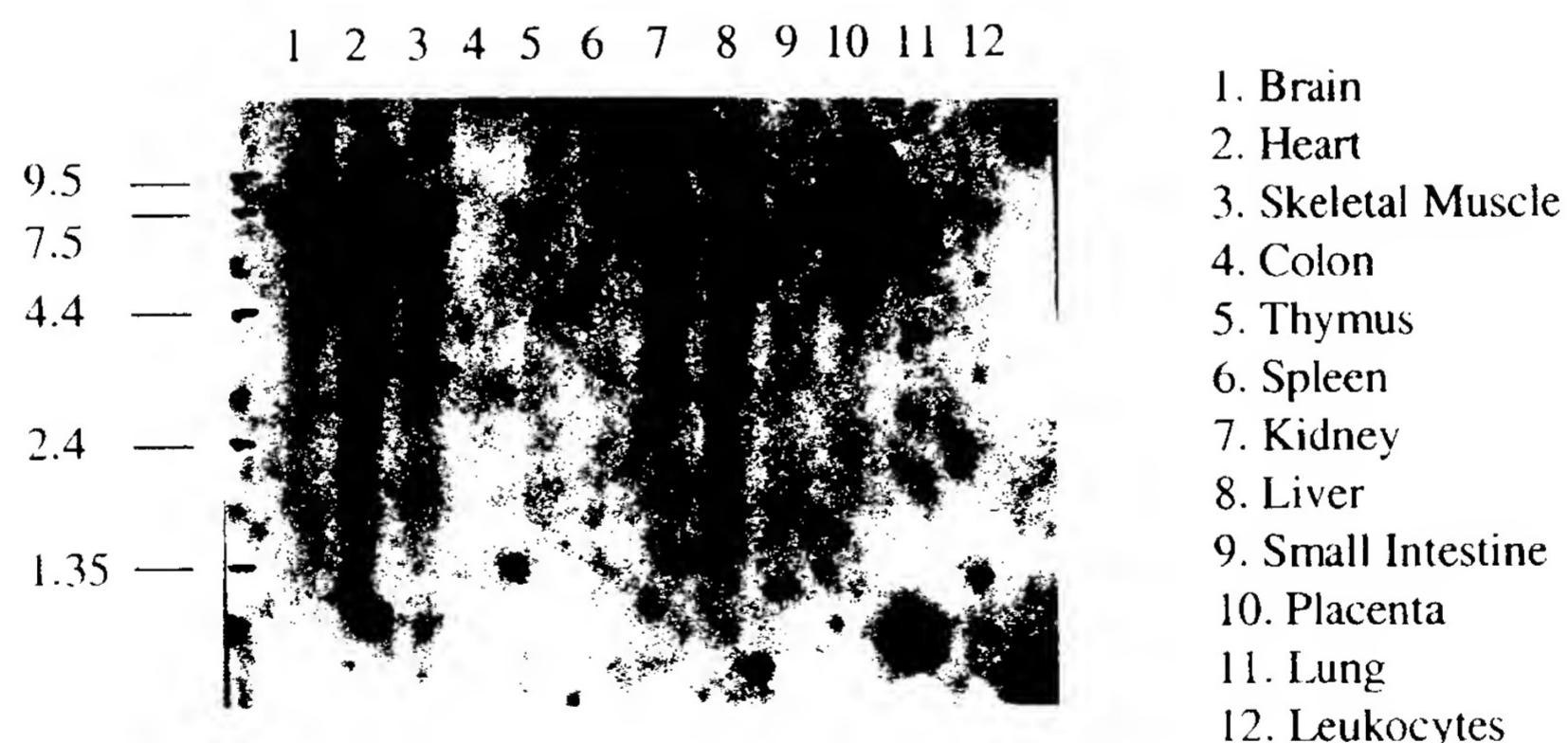


FIG. 6L

Gene 605



Gene 606

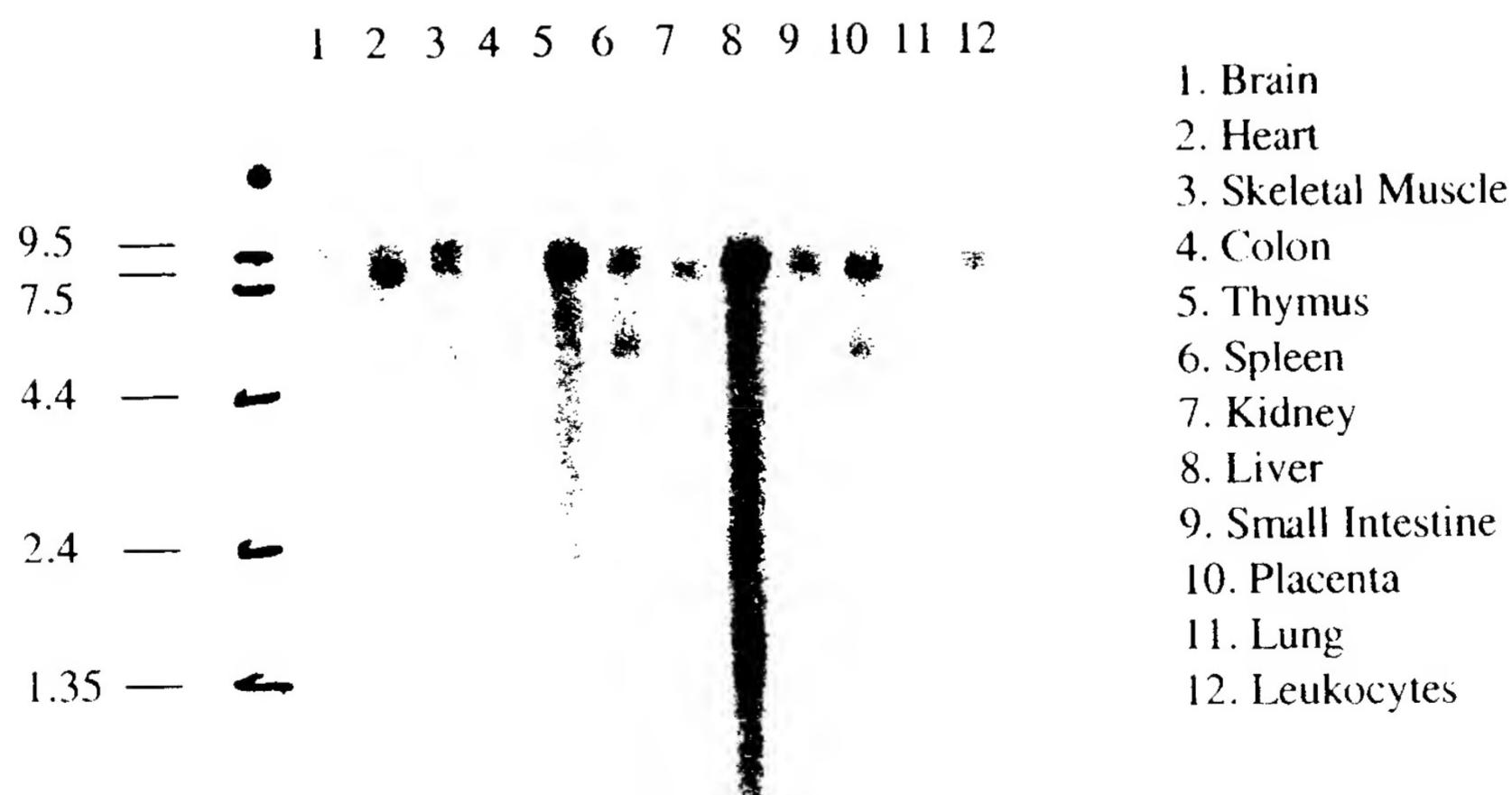
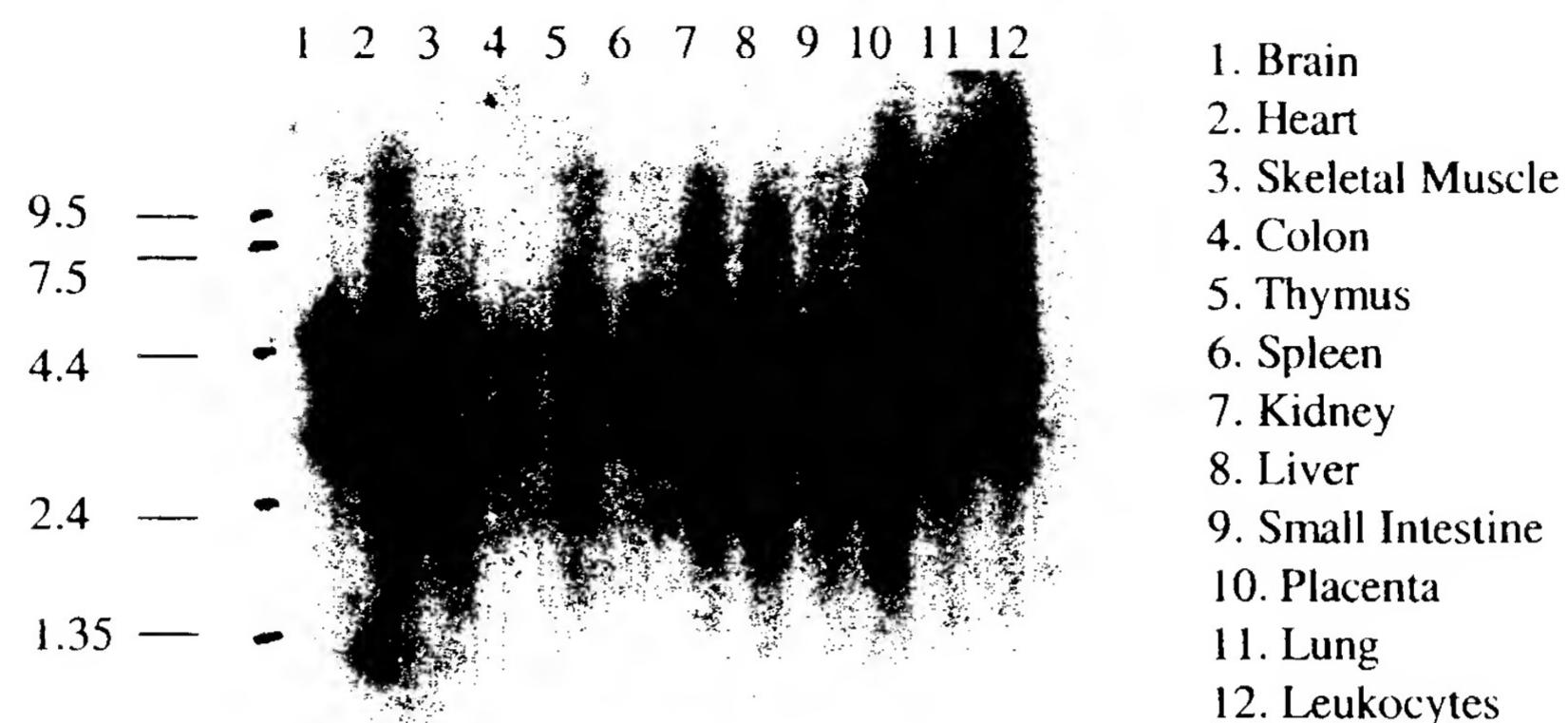


FIG. 6M

Gene 608

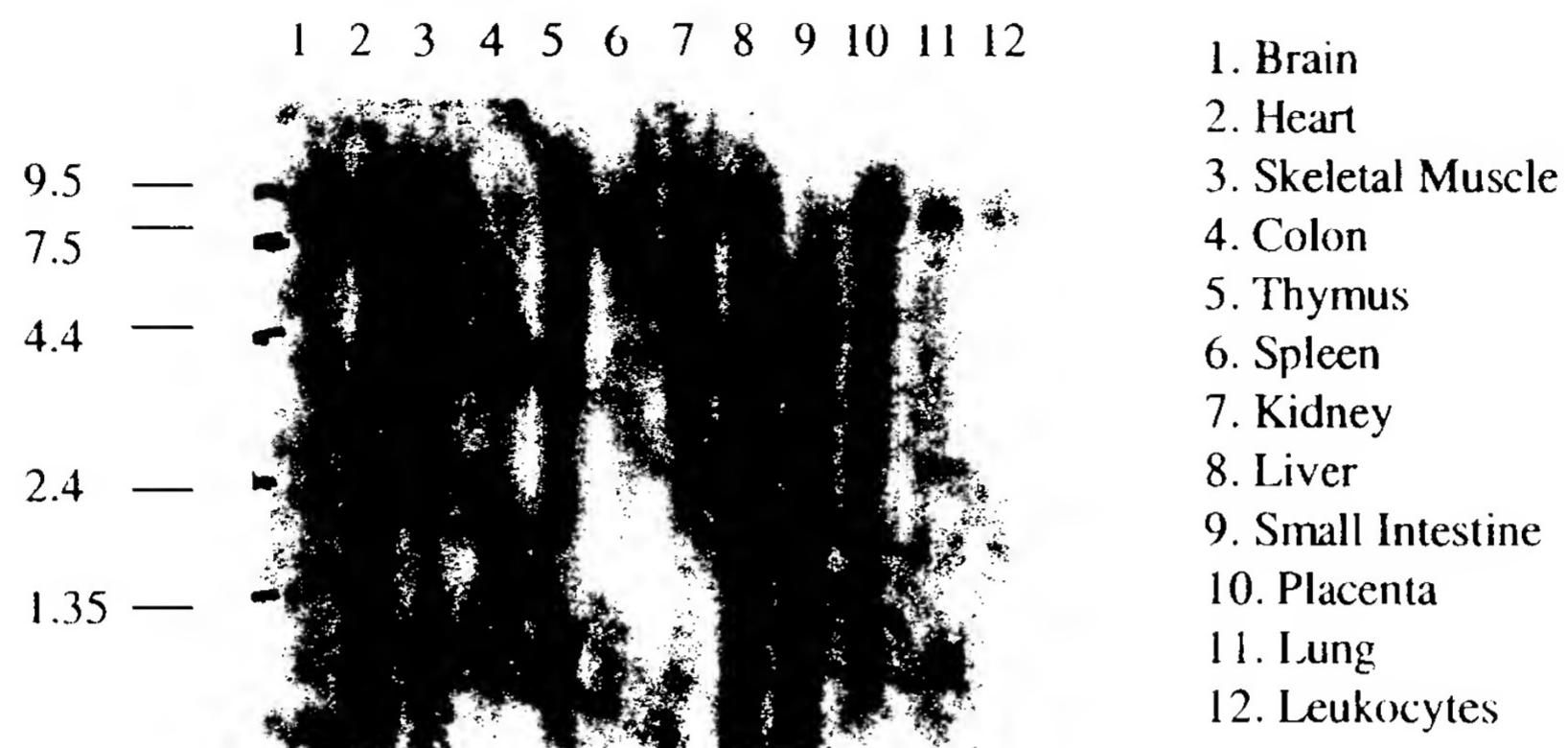


Gene 611



FIG. 6N

Gene 615



Gene 617

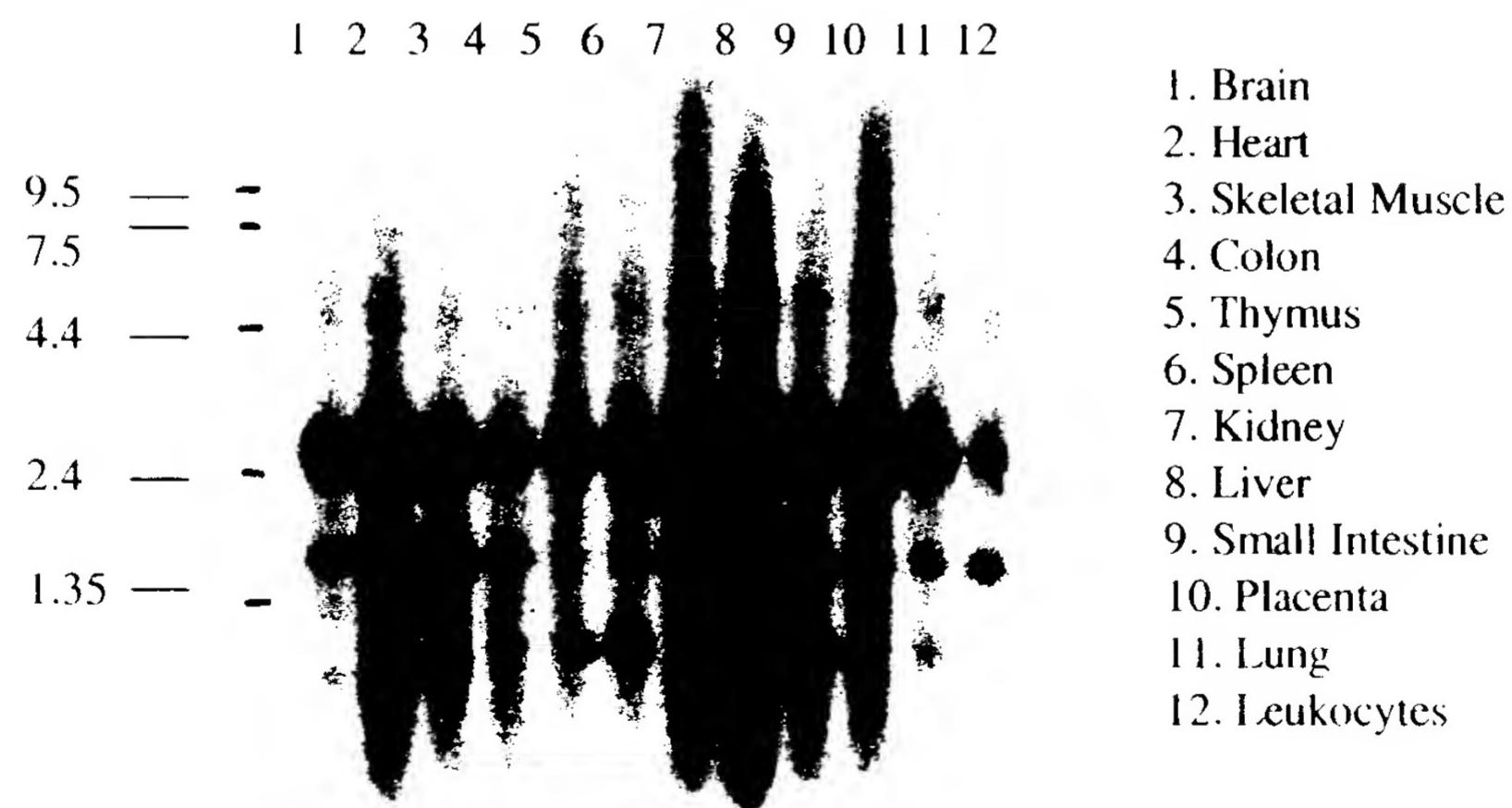
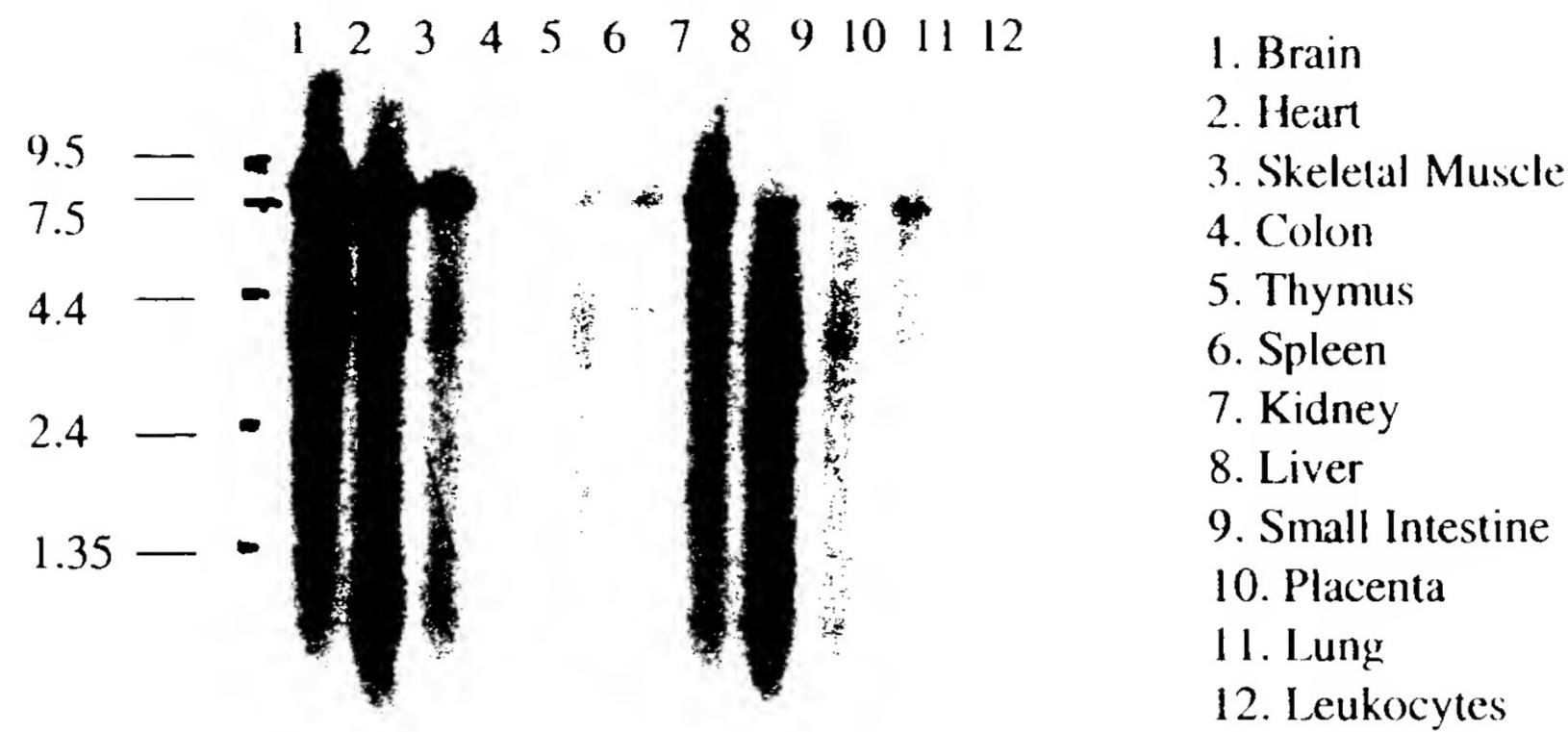


FIG. 60

Gene 618



Gene 619

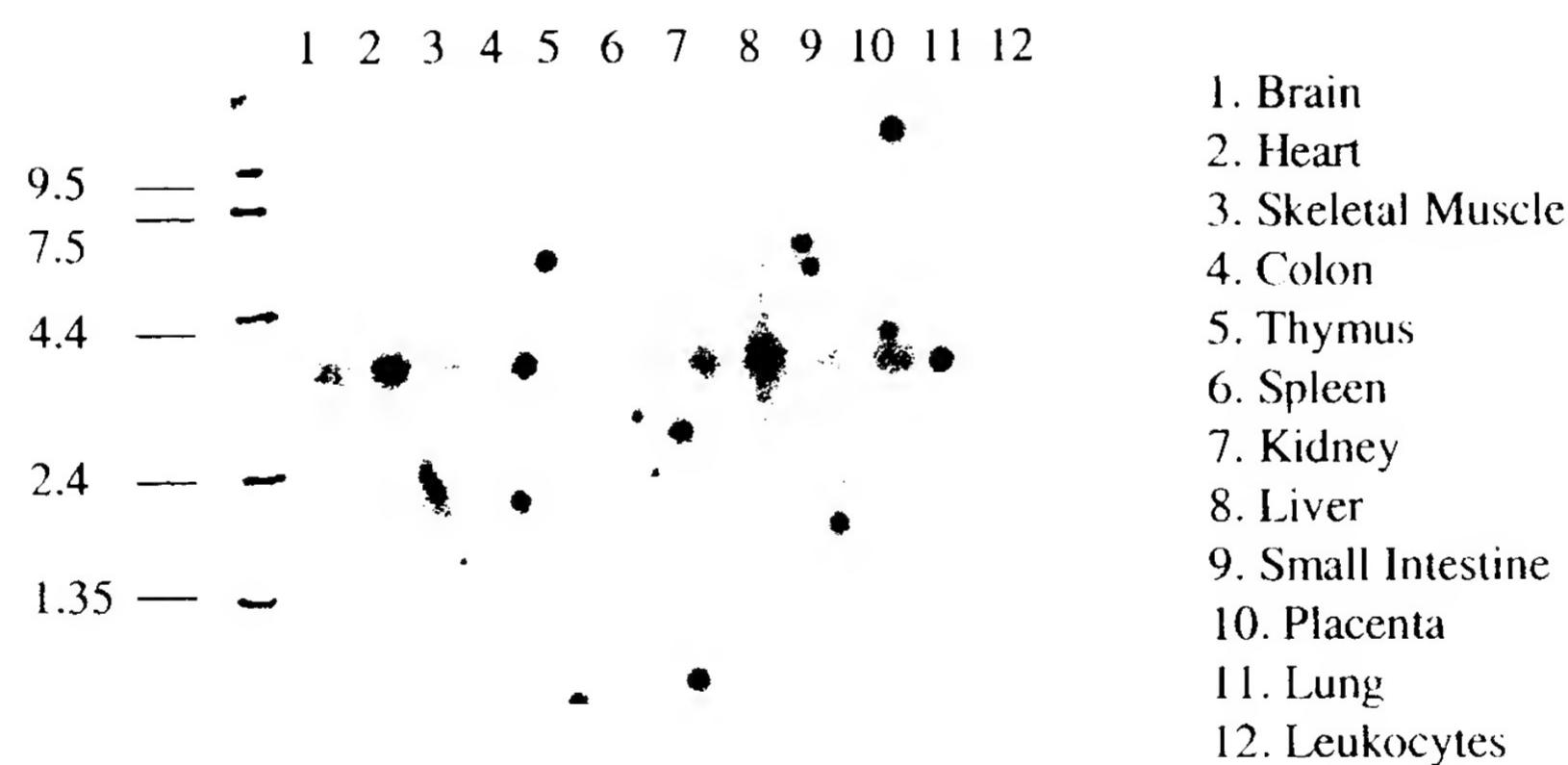
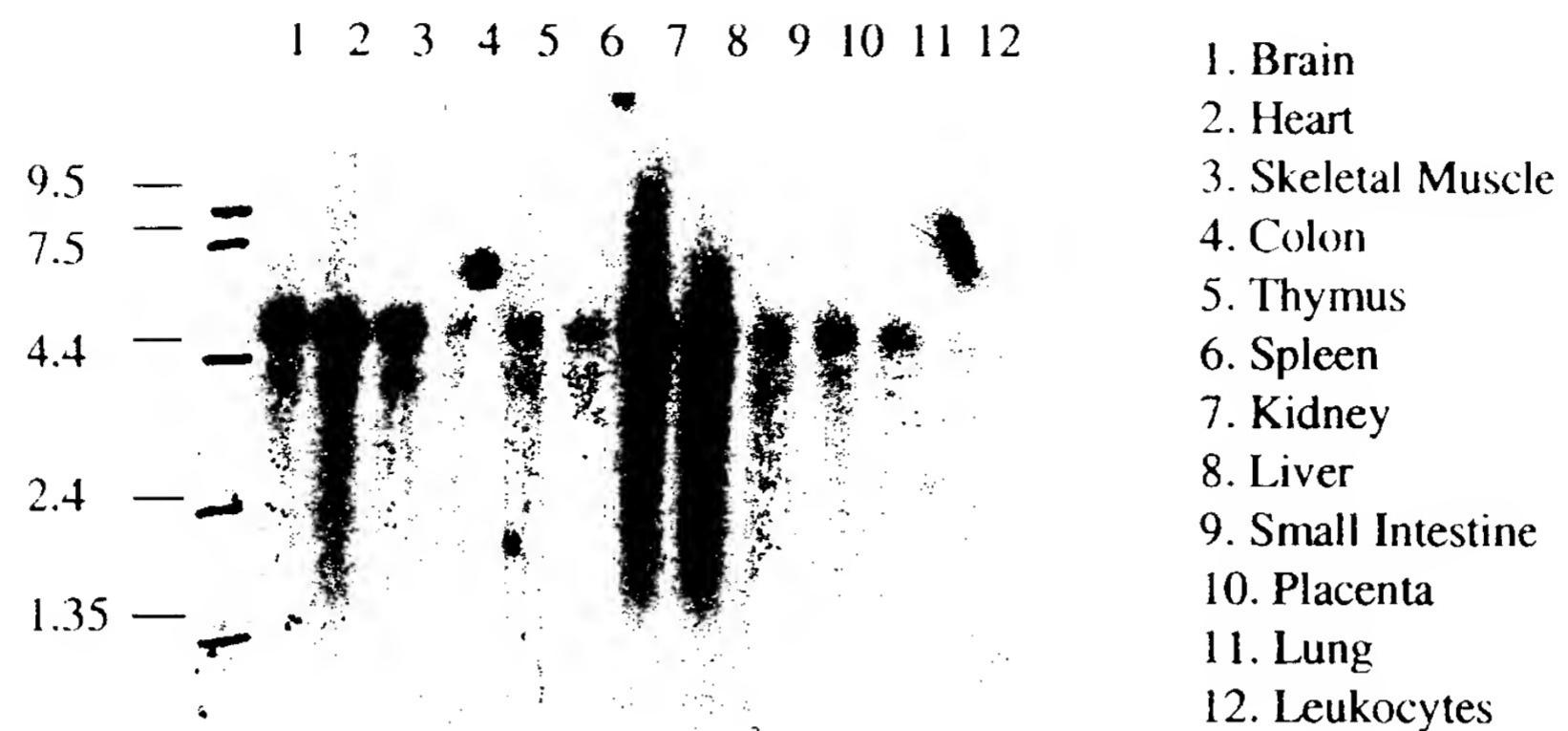


FIG. 6P

Gene 621



Gene 693

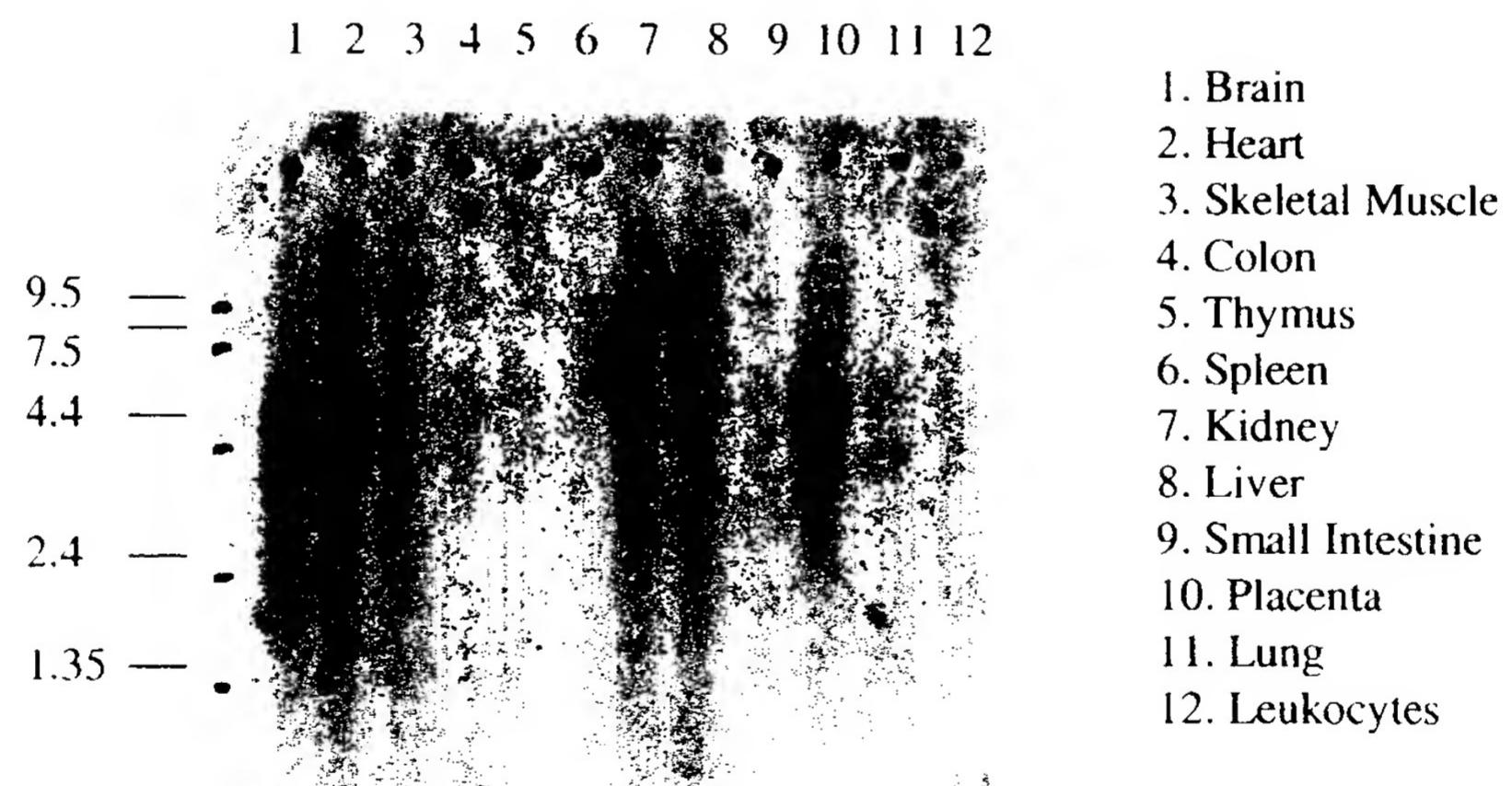
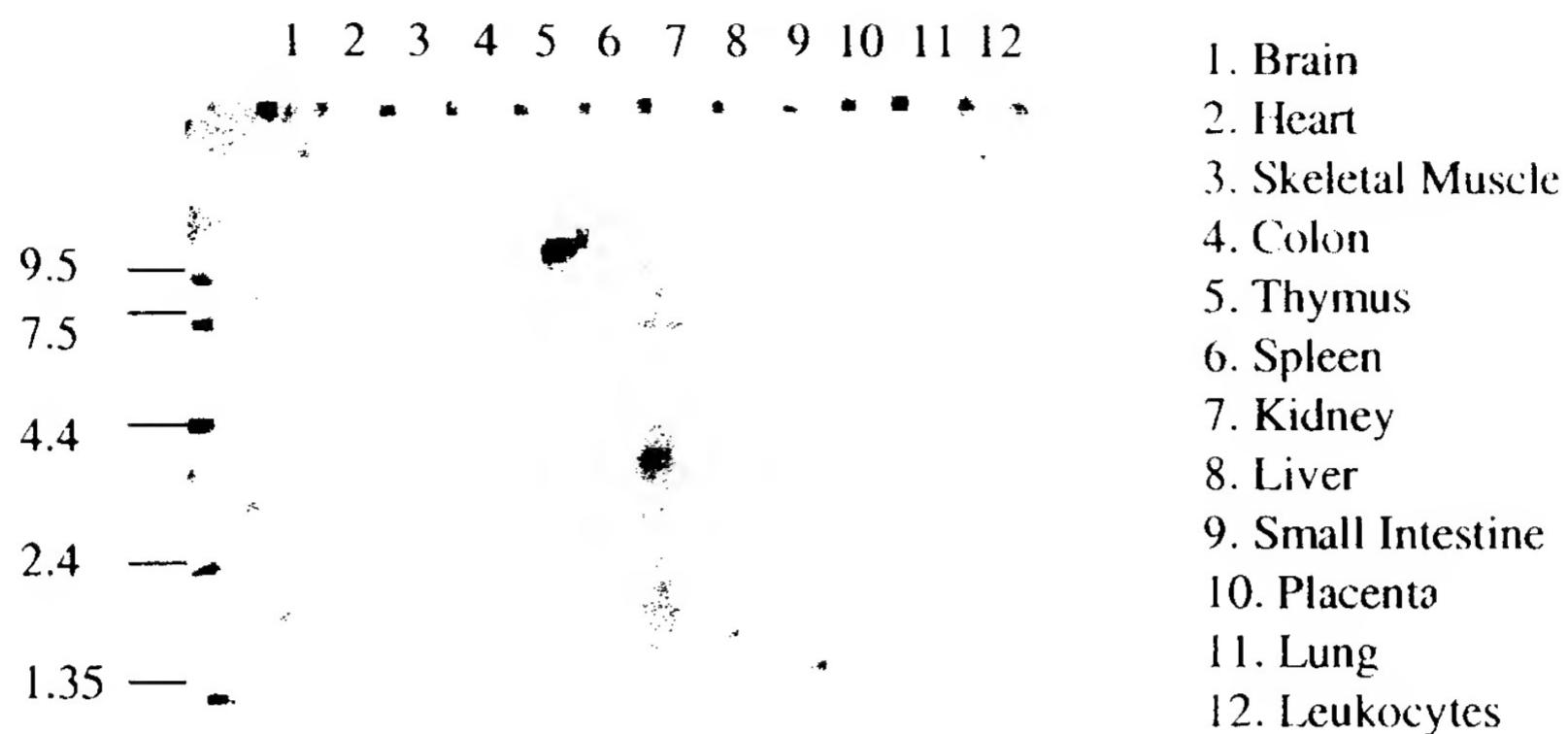


FIG. 6Q

Gene 698



Gene 699

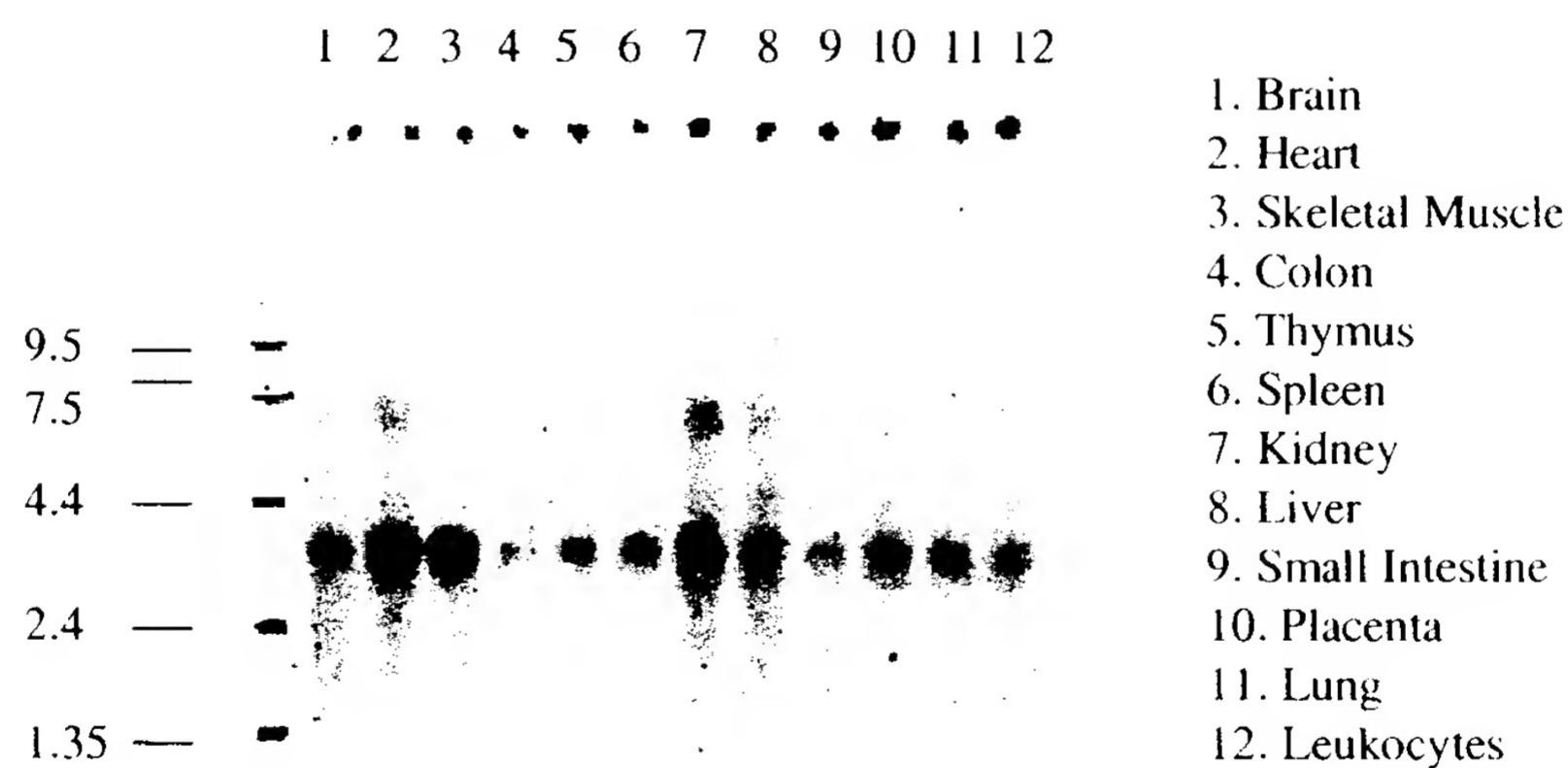
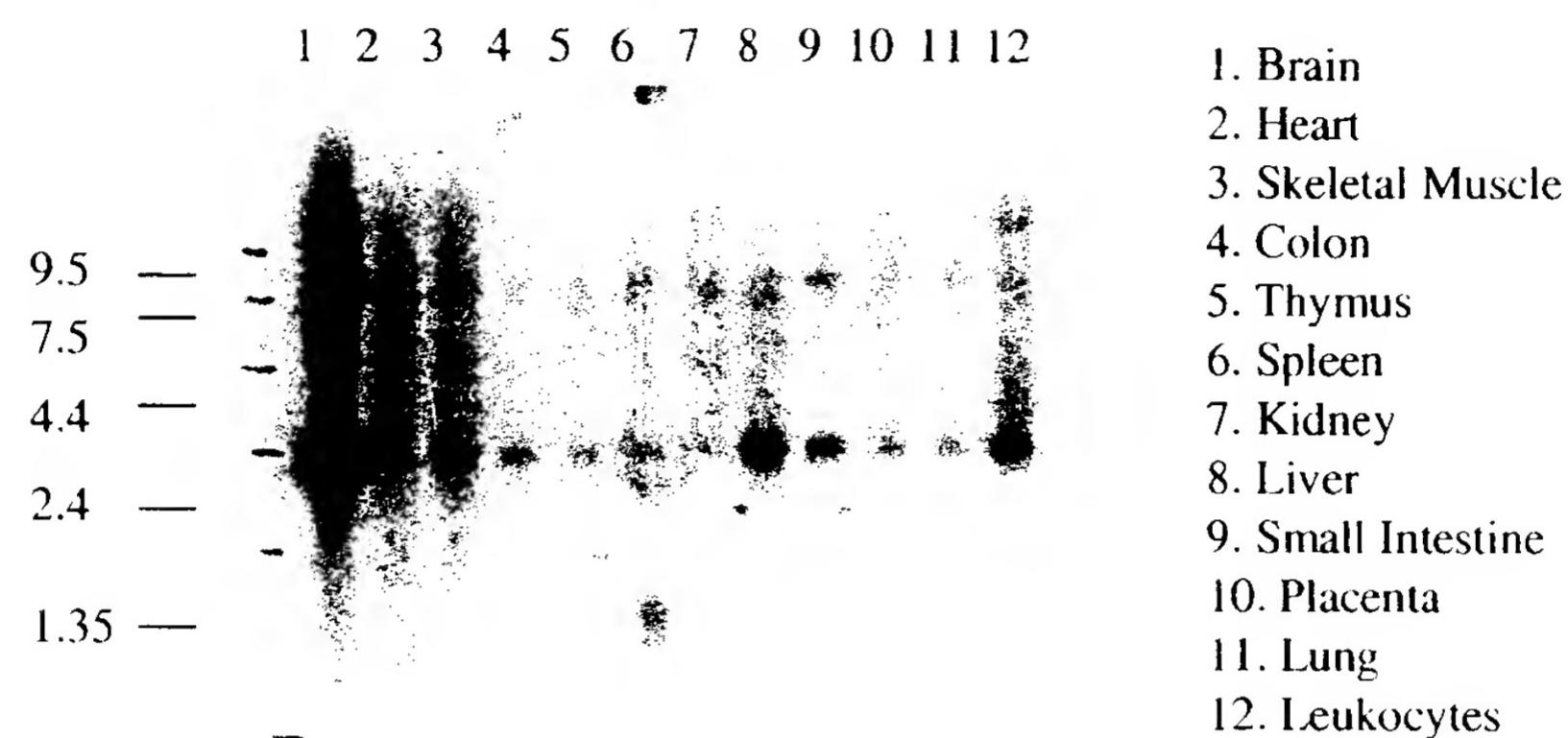


FIG. 6R

Gene 702

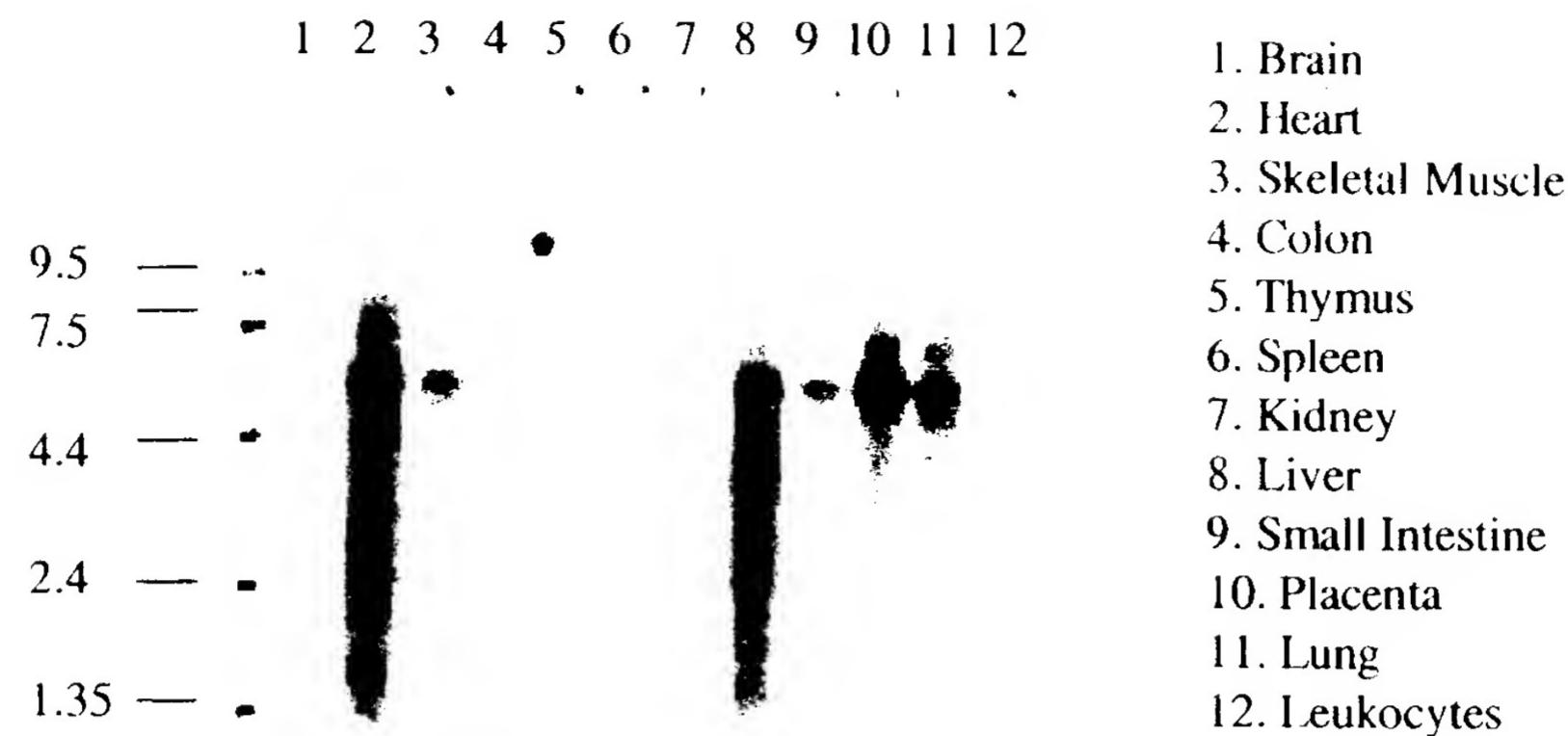


Gene 722



FIG. 6S

Gene 751



Gene 756

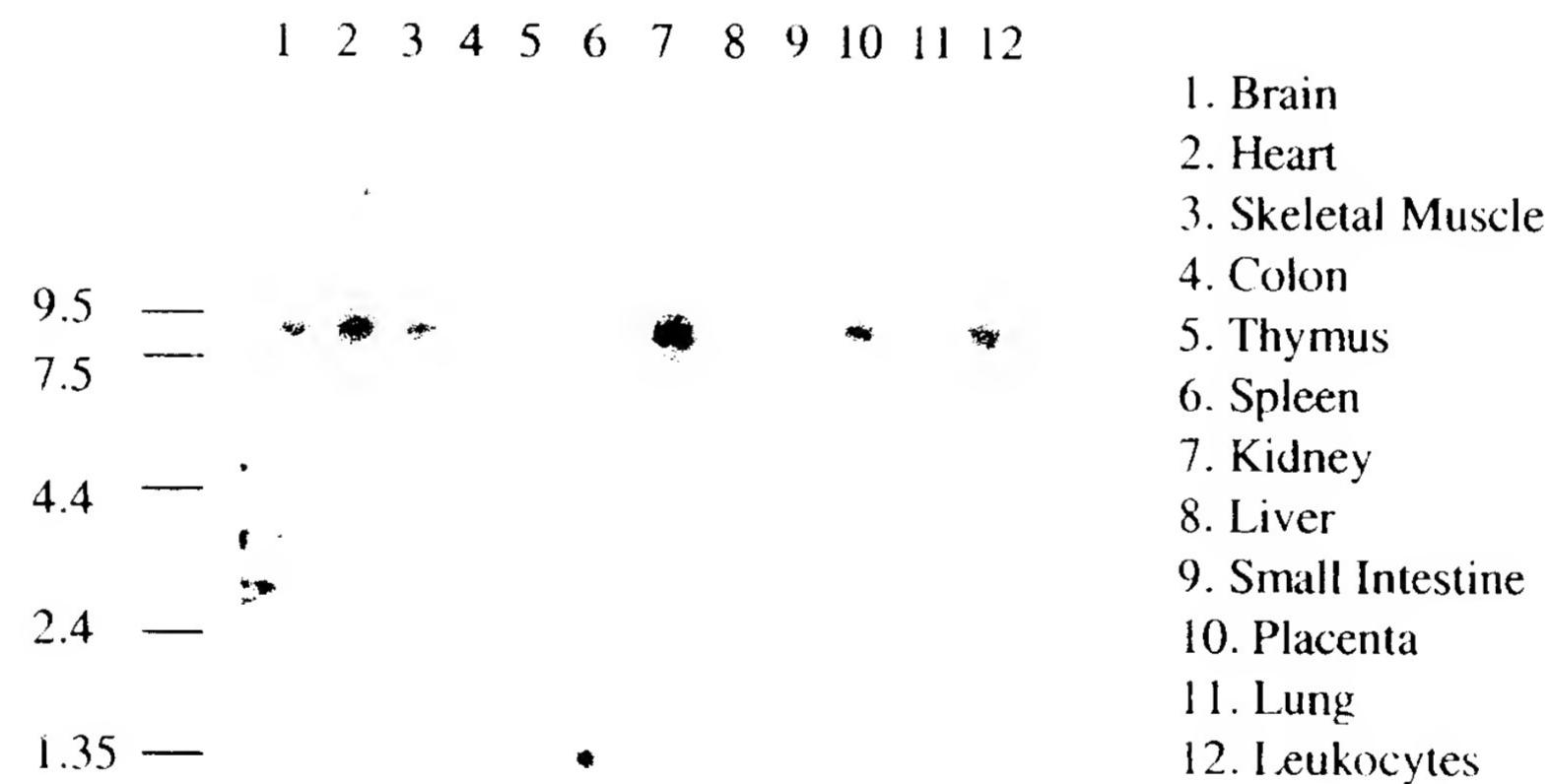
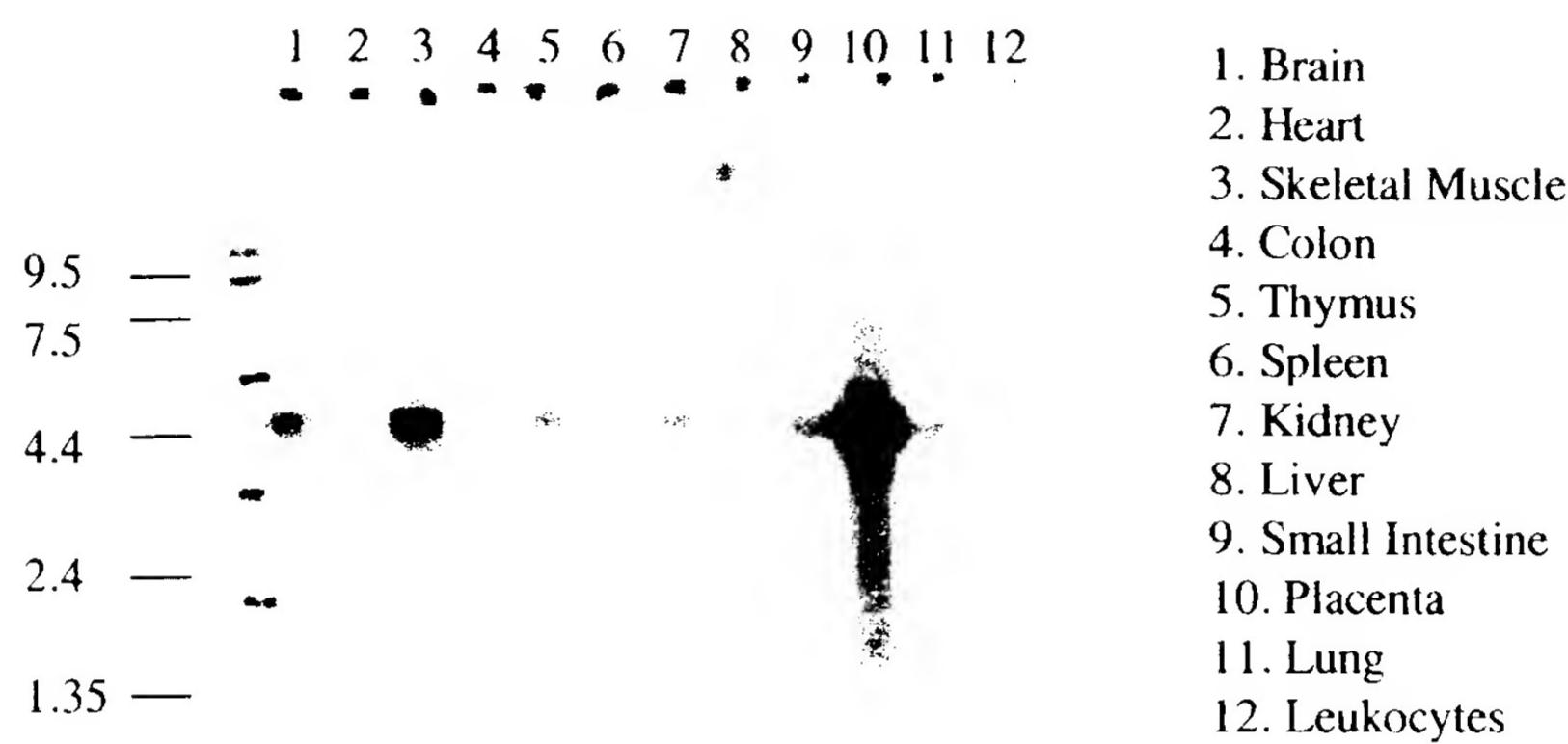


FIG. 6T

Gene 757



Gene 848

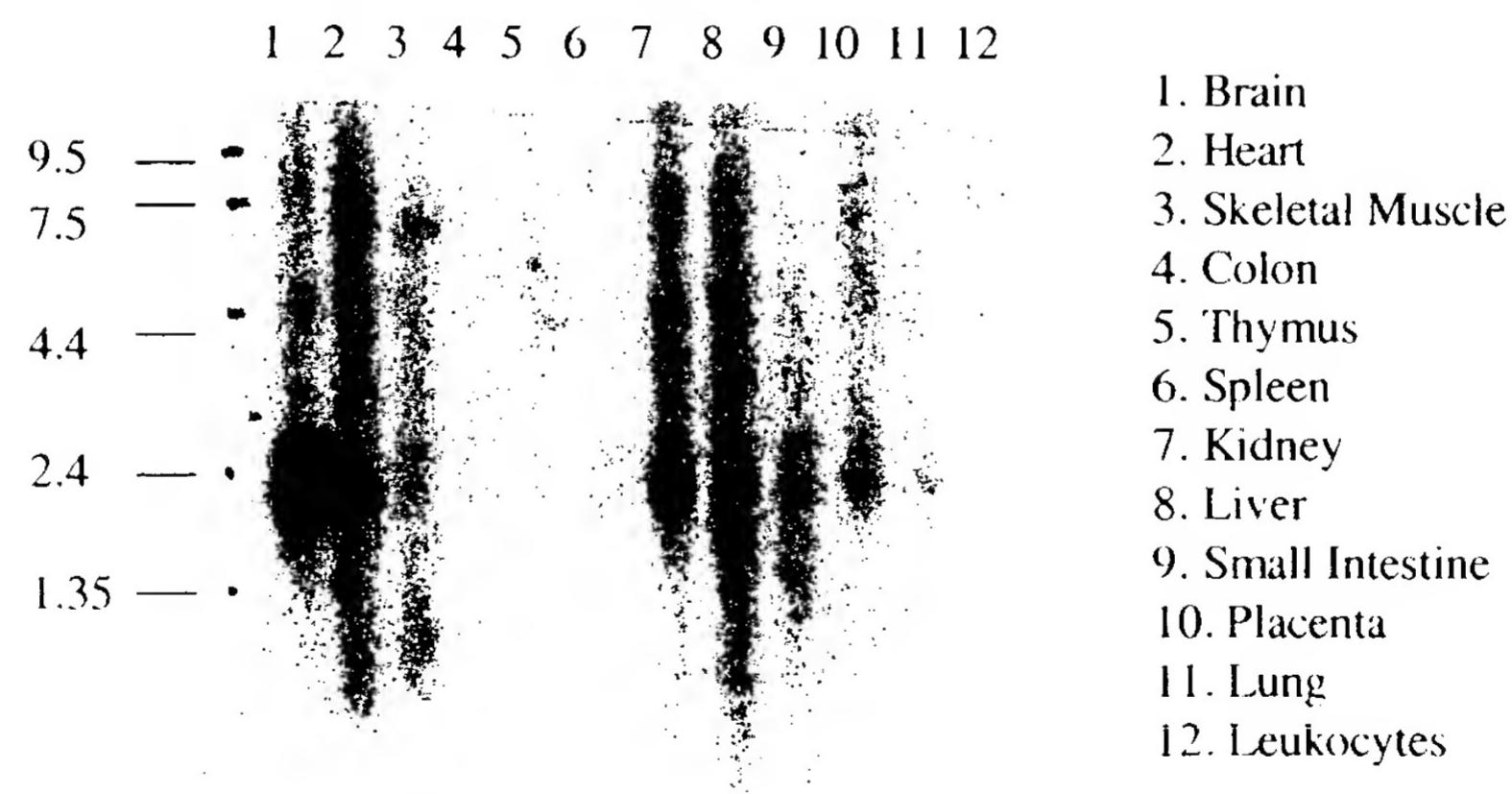


FIG. 6U

10	30	50
GCTTGCTGTGGCCCTGTCAGGAAGAGTAGAGCTCTGGTCCAGCTCCGCGCAGGGAGGGAG		
70	90	110
GCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTCCAGTATGAGACGAACAAA MetProAlaCysCysSerCysSerAspValPheGlnTyrGluThrAsnLys		
130	150	170
GTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTTCCACGTGATCATC ValThrArgIleGlnSerMetAsnTyrGlyThrIleLysTrpPhePheHisValIleIle		
190	210	230
TTTCCTACGTTGCTTGCTCTGGTAGTGACAAGCTGTACCGCGAAAGAGCCTGTC PheSerTyrValCysPheAlaLeuValSerAspLysLeuTyrGlnArgLysGluProVal		
250	270	290
ATCAGTTCTGTGCACACCAAGGTGAAGGGATAGCAGAGGTGAAAGAGGGAGATCG <u>TGGAG</u> IleSerSerValHisThrLysValLysGlyIleAlaGluValLysGluGluIle <u>Val</u> Glu		
310	330	350
AATGGAGTGAAGAAGTTGGTGCACAGTGTCTTGACACCGCAGACTACACCTCCCTTG AsnGlyValLysLysLeuValHisSerValPheAspThrAlaAspTyrThrPheProLeu		
370	390	410
CAGGGAACTCTTCTTCGTATGACAAACTTCTAAAACAGAAGGCCAAGAGCAGCGG GlnGlyAsnSerPhePheValMetThrAsnPheLeuLysThrGluGlyGlnGluGlnArg		
430	450	470
TTGTGTCCCAGTATCCCACCCGCAGGACGCTCTGTTCTCTGACCGAGGTGTAAAAAG LeuCysProGluTyrProThrArgArgThrLeuCysSerSerAspArgGlyCysLysLys		
490	510	530
GGATGGATGGACCCGCAGAGCAAAGGAATTCAAGACCGGAAGGTGTAGTGCATGAAGGG GlyTrpMetAspProGlnSerLysGlyIleGlnThr <u>Gly</u> ArgCysValVal <u>His</u> GluGly		
550	570	590

FIG. 7A

AACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGAAAGAGGCC
AsnGlnLysThrCysGluValSerAlaTrpCysProIleGluAlaValGluGluAlaPro

610

630

650

CGGCCTGCTCTCTTGAAACAGTGCCGAAAACTTCACTGTGCTCATCAAGAACAAATATCGAC
ArgProAlaLeuLeuAsnSerAlaGluAsnPheThrValLeuIleLysAsnAsnIleAsp

670

690

710

TTCCCCGGCCACAACTACACCACGAGAAACATCCTGCCAGGTTAAACATCACTTGTAC
PheProGlyHisAsnTyrThrThrArgAsnIleLeuProGlyLeuAsnIleThrCysThr

730

750

770

TTCCACAAGACTCAGAATCCACAGTGTCCCATTTCGACTAGGAGACATCTCCGAGAA
PheHisLysThrGlnAsnProGlnCysProIlePheArgLeuGlyAspIlePheArgGlu

790

810

830

ACAGGCGATAATTTCAGATGTGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTAC
ThrGlyAspAsnPheSerAspValAlaIleGlnGlyGlyIleMetGlyIleGluIleTyr

850

870

890

TGGGACTGCAACCTAGACCGGTTCCATCACTGCCGTCCAAATACAGTTCCGTCGC
TrpAspCysAsnLeuAspArgTrpPheHisHisCysArgProLysTyrSerPheArgArg

910

930

950

CTTGACGACAAGACCACCAACGTGTCCTTGTACCCGTACAAACTTCAGATACGCCAAG
LeuAspAspLysThrThrAsnValSerLeuTyrProGlyTyrAsnPheArgTyrAlaLys

970

990

1010

TACTACAAGGAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTCGGGATCCGTTT
TyrTyrLysGluAsnAsnValGluLysArgThrLeuIleLysValPheGlyIleArgPhe

1030

1050

1070

GACATCCTGGTTTGGCACCGGAGGAAATTGACATTATCCAGCTGGTTGTACATC
AspIleLeuValPheGlyThrGlyGlyLysPheAspIleIleGlnLeuValValTyrIle

1090

1110

1130

GGCTCAACCCTCTCCTACTTCGGTCTGGCCACTGTGTTCATCGACTCCTCATCGACACT
GlySerThrLeuSerTyrPheGlyLeuAlaThrValPheIleAspPheLeuIleAspThr

1150

1170

1190

TACTCCAGTAACGTGCTCGCTCCCATATTATCCCTGGTGCAAGTGCTGTCAGCCCTGT
 TyrSerSerAsnCysCysArgSerHisIleTyrProTrpCysLysCysCysGlnProCys

1210

1230

1250

GTGGTCAACGAATACTACTACAGGAAGAAGTGCAGTCATTGTGGAGCCAAAGCCGACA
 ValValAsnGluTyrTyrArgLysLysCysGluSerIleValGluProLysProThr

1270

1290

1310

TTAAAGTATGTGTCCTTGATGAATCCCACATTAGGATGGTGAACCAGCAGCTACTA
 LeuLysTyrValSerPheValAspGluSerHisIleArgMetValAsnGlnGlnLeuLeu

1330

1350

1370

GGGAGAAGTTGCAAGATGTCAAGGGCCAAGAACGACTCCAAAGACCTGCGATGGACTTCACA
 GlyArgSerLeuGlnAspValLysGlyGlnGluValProArgProAlaMetAspPheThr

1390

1410

1430

GATTGTCCAGGCTGCCCTGGCCCTCCATGACACACCCCCGATTCTGGACAACCAGAG
 AspLeuSerArgLeuProLeuAlaLeuHisAspThrProProIleProGlyGlnProGlu

1450

1470

1490

GAGATACAGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAGCCCCGTCTGGTGC
GluIleGlnLeuLeuArgLysGluAlaThrProArgSerArgAspSerProValTrpCys

1510

1530

1550

CAGTGTGGAAGATGCCTCCATCTCAACTCCCTGAGAGCACAGGTGCCTGGAGGAGCTG
 GlnCysGlyArgCysLeuProSerGlnLeuProGluSerHisArgCysLeuGluLeu

1570

1590

1610

TGCTGCCGGAAAAAGCCGGGGCCTGCATCACCACTCAGAGCTGTTAGGAAGCTGGTC
 CysCysArgLysLysProGlyAlaCysIleThrThrSerGluLeuPheArgLysLeuVal

1630

1650

1670

CTGTCCAGACACGTCTGCAGTTCTCTGCTCTACCAGGAGCCCTGCTGGCGCTGGAT
 LeuSerArgHisValLeuGlnPheLeuLeuTyrGlnGluProLeuLeuAlaLeuAsp

1690

1710

1730

FIG. 7C

GTGGATTCCACCAACAGCCGGCTGCGGCAGTGTGCCTACAGGTGCTACGCCACCTGGCGC
ValAspSerThrAsnSerArgLeuArgHisCysAlaTyrArgCysTyrAlaThrTrpArg

1750

1770

1790

TTCGGCTCCCAGGACATGGCTGACTTGCCCATCCTGCCAGCTGCTGCCGCTGGAGGATC
PheGlySerGlnAspMetAlaAspPheAlaIleLeuProSerCysCysArgTrpArgIle

1810

1830

1850

CGGAAAGAGTTCAAAGAGTGAAGGGCAGTACAGTGGCTTAAGAGTCCTTACTGAAGC
ArgLysGluPheProLysSerGluGlyGlnTyrSerGlyPheLysSerProTyrEnd

1870

1890

1910

CAGGCACCGTGGCTCACGTCTGTAATCCCAGCGCTTGGGAGGCCAGGCAGATCA

1930

1950

1970

CCTGAGATCGGGAGTTGGAGACCCGCCTGGCTAACAAAGGCGAAATCCTGTCTGTACTAAA

1990

2010

2030

AATACAAAAATCAGCCAGACATGGTGGCATGCACCTGCAATCCCAGCTACTCGGGAGGCT

2050

2070

2090

GAGGCACAAGAATCACTTGAACCCGGGAGGCAGAGGTTGTAGTGAGCCCAGATTGTGCCA

2110

2130

2150

CTGCTCTCCAGCCTGGAGGCACAGCAAACTGTCCCCAAAAAAAAAGAGTCCTTAC

2170

2190

2210

CAATAGCAGGGCTGCAGTAGCCATGTTAACATGACATTACAGCAACTTGAACCTCAC

2230

2250

2270

CTGCAAAGCTCTGTGGCACATTTCAGCCAAGGGAAATATGCTTCATCTTCTGTTGC

2290

2310

2330

TCTCTGTCTGAGAGCAAAGTGACCTGGTAAACAAACCAGAATCCCTACATGGACT

2350

2370

2390

FIG. 7D

CAGAGAAAAGAGATTGAGATGTAAGTCTCAACTCTGTCCCCAGGAAGTTGTGTGACCTA
2410 2430 2450
GGCCTCTCACCTCTGTGCCTCTGTCTCCTTGTGCCAACTACTATCTCAGAGATATTGT
2470 2490 2510
GAGGACAAATTGAGACAGTCACATGAACGTCTTTAATGTGTAAAGATCTACATGAAT
2530 2550 2570
GCAAAACATTCATTATGAGGTCAAGACTAGGATAATGTCCAACAAAAACAAACCCTTT
2590 2610 2630
CATCCTGGCTGGAGAACATGGAGAACTAAAGCTGGCCACAAATTCTTGACACTCAAGTC
2650 2670 2690
CCCCAAGACCTAAGGGTTTATCTCCTCCCTTGAATATGGGTGGCTCTGATTGCTTAT
2710 2730 2750
CCAAAAGTGGAAAGTACATTGTGTCAGTTCACTGATCTTAAGAGGCTGACAGCTT
2770 2790 2810
CTACTTGCTGTCCCTGGAACTCTGCTATCGGGGAAGCCAGACGCCATTAAAAGTCTG
2830 2850 2870
CCTATCCTGGCCAGGTGTGGTGGCTCACACCTGTAATCCCAGCAGCTTGGGAGACCAAGG
2890 2910 2930
CGGGCGGATCACTAAAGTCAGGAGTCCAAGACCAGACTGCCAACATGGTGAAACCGTA
2950 2970 2990
TCTCTAATAAAAATACAAAAATTAGCTGGGCATGGTGCAGGCACCTGTAGTCCTAGCTAT
3010 3030 3050
CAAGAGGGCTGAGACAGGGAGAAACACTTGAACCTGGGAGGTGGAGGTTGCATTGAGCTGAG

3070 3090 3110
ATCGTGCCACTGCACTCCAGGCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAAAAAA
3130 3150 3170
AAAAGAAAAAAATGTCTGCCTATCCTGAGACTGCCCTGCTGTGAGGAAGCCCAAGCA
3190 3210 3230
GTCACGTGGACAGTGCCTGACCAGCCCCAGCTTCAAGCCATCCAAGCCCAGTCACCAA
3250 3270 3290
CATGAGAGAGAAGAACCTTCAGGTGATTCTGGACTCCACTAACATATGACTGATAACGC
3310 3330 3350
ATGATAACATCCAAAGTGAGAACTGCCCATAAATCCAGAAAACCACATTGCTATCTTAAG
3370 3390 3410
TCCCTAAGTTGGGCTTATTGTTCCACAGCAACAGGTAACGGAACAGAGGGCAAGCC
3430 3450 3470
TGATGAATGGGCACACAGACTCAGCCCACCTCCCTGGTTCTAATGTTCTCAGGGAGC
3490 3510 3530
CCGGACCAACCCTGGGAGCCTCAGGAACCTAGGTTCCACTGGACAGTTCTAGAAGGGCT
3550 3570 3590
ATAGACCAAATCAGGTAACTCACCAGACCAGCCTGGAATCTATCAAATCTAACTGCTGA
3610 3630 3650
GCTACCCAGTGCATTCCGATCCTCATCACAAATTCTTGACTGAAGGCCGGCGTGGTGGC
3670 3690 3710
TCACGCCTGTAATCCCAGCCTTGGAGGCTGAGGCGGGTGGATCACCTGAGGTAGGA

FIG. 7F

3730 3750 3770
GTTCGAGACCAGCCTGGCCAACATGGTGAGACCCCTGTCTACTAAGAACAAAAATTAA

3790 3810 3830
GGTGGGGTGGCGGTGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAAC

3850 3870 3890
TCTTGAACCTGGAAGGTGGAGGTTGCAATAAGCCGAGATAAGTGCCTACTGCAC

3910 3930 3950
AGATAACAGAGCAAGACTCTGTCTAAAAAACACAACAACAACAAAACAATTCTAT

3970 3990 4010
GACTGAAAGTGA

4030 4050 4070
ACTAAAAAGCTGGCTTATGCCATTAACACTCTGTACTTTGCAGCCAAT

4090 4110 4130
CAGAACTGACGCAGTCTGGGTGCTAGCTGCTTC

4150 4170 4190
AAAGCAACCCACACCACACTTTACC

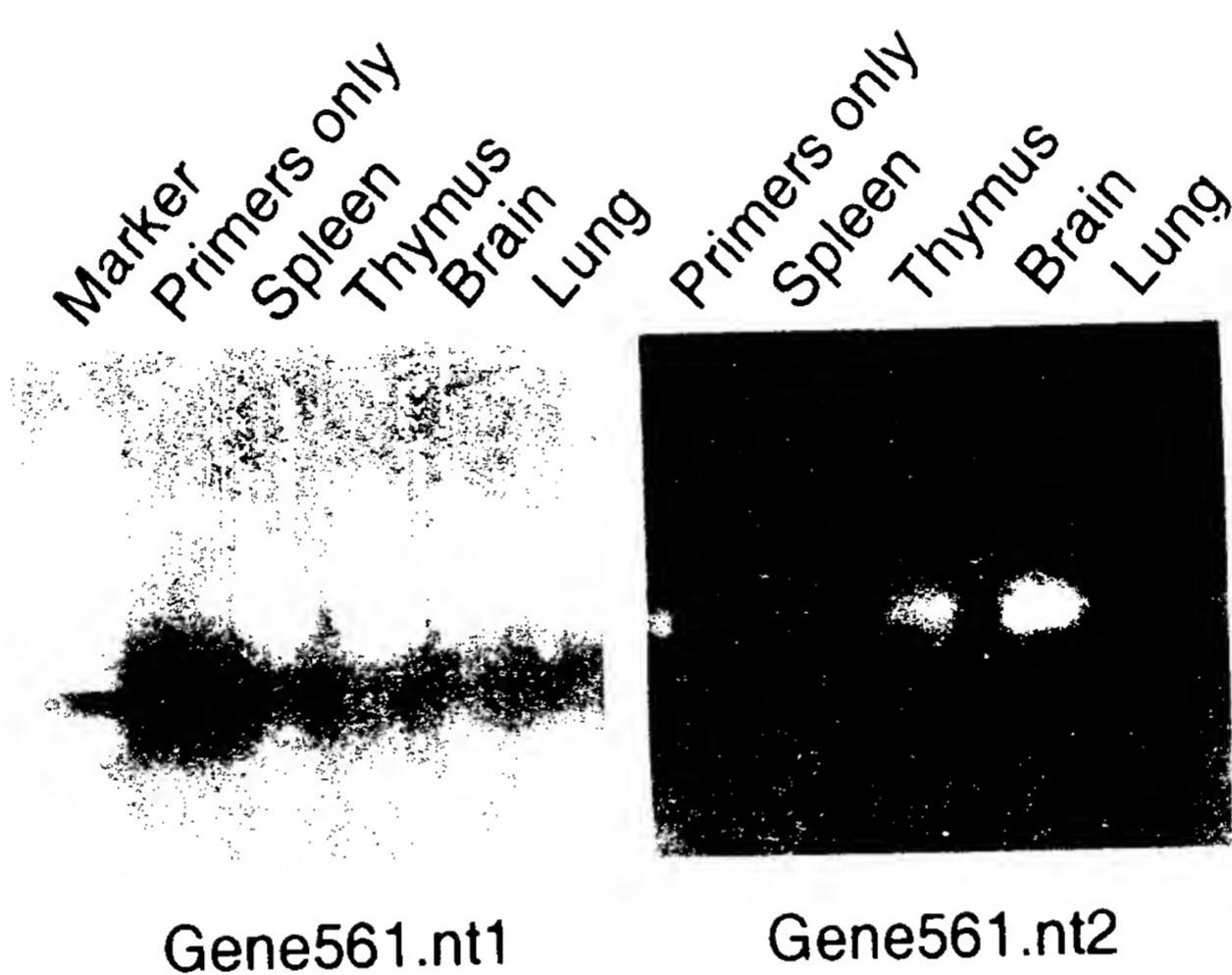
4210 4230 4250
CTTCAGGATTCCCTTCCCTGGTTGGTCACTAGAGTTGGCTATTATCTGTTCTAAC

4270 4290 4310
AATAGCTATTTATCGAATAGTTAGAGACCCTATTAAATATTGTGACTGATGAAGGAT

4330 4350 4370
CTGTGAATTTTATATGTTCTAAGAGTTACCATTTGATACCTTAAAC

4390 4410 4430
AGCTTCTACTATATTCA

TATTTGGCTTAAACTCAGGAACCAAGTTAATTATGCCAGATTGAACTTGATTTACT
4450 4470 4490
ACCTTTCAAAGATATTTAAAAAGTGGATTACTACATATGATTCTTGGAGCTTACAT
4510 4530 4550
TTCTTACTTCACGAATTCTATGTCACTGTTACAAGTTCCATTCTGATGGCTCTGGC
4570 4590 4610
CTTGACCTTGTGTTGGTGCCTTATTCTAGTATGTTCTATCACCTTAATGAGGCC
4630 4650 4670
GCAGATGGAGTCAGAATGTGAAATTACAAATAATCACTGGATCCATCTACTGTTCCAT
4690 4710 4730
CACCTCCCCACTGATGCTCTGGCGAGAGAGTGATGTGTCACCTCAACTGTGTGTAATA
4750 4770 4790
TGTCAGACACGTCCCTACAATAACAGGCGTCATATTGTATTATTTAGTTACTGTAGA
4810 4830 4850
AAATAATGTCACCGCCAAAGGTGATGAGAGTCACGTTGTAGGATCTGTTCTTATAC
4870 4890 4910
TTAAAGACAGACTCTGCTACGTAATTGCCAGTATTGCTTGTGTCAGA
4930 4950 4970
AGAGAAGGGATCTGCTTCTTGGCTGATTCACATAGCATTGTAATAGACATGCATT
4990 5010 5030
TCTCTTCTAAAGGGAGTAACCTTAAACCCTCCTGATTTAGCCTGGCAATGTAAG
5050 5070
TGTCCTTAATGTGACTGTTTGATAATTAAAAAAAGGTATATAATT



RT/PCR of Gene561.nt1 and Gene561.nt2

FIG. 8

10 30 50
TCGAAACAGCTGCCGGCTGGTCCC GGCGAGGCCGGCGCAGGGAGGGAGGAGCCGCCGG

70 90 110
GCTGTGGGGCGCCCGAGCTGGGCCGGCTCGGTGTGCCCGCCGCCAGCCCGCTCCA

130 150 170
GACGCGCCACCTGGCGCTCCAAGAAGAGGCCGAAGTTGCCGCCGTGAGTTGGAGC

190 210 230
TCGCGCCGGGCCGCTGCGCCGGAGCTCCGGGGCTTCCTCGCTTCCGGTATTGTTG

250 270 290
CAAACTTGCTGCTCTCCGCCGCCGGCCCCAACTCGCGGACGCCGGCGGGAGGCCG

310 330 350
AGCCGGGGCGCTGTGCGCAGCGCTGGGCCAGGCCGGGGCATGGCGGGGCCGA

370 390 410
GCAGGGGTGGAGAGGCCGGGCCAGCAGCAGGCCGTGCCCGGGAGCGGCCGGCTGAGGG

430 450 470
CGCGGAGCTCCCCCGAGGACACGTCCAACGCCAGCATGCAGGCCGGCCCCGCCCTG
MetGlnArgProGlyProArgLeu

490 510 530
TGGCTGGTCTGCAGGTGATGGCTCGTGCGCCATCAGCTCCATGGACATGGAGCGC
TrpLeuValLeuGlnValMetGlySerCysAlaAlaIleSerSerMetAspMetGluArg

550 570 590
CCGGGCGACGGCAAATGCCAGCCCATCGAGATCCCGATGTCAAGGACATCGGCTACAAC
ProGlyAspGlyLysCysGlnProIleGluIleProMetCysLysAspIleGlyTyrAsn

610 630 650

FIG. 9A

ATGACTCGTATGCCAACCTGATGGGCCACGAGAACCGCGAGGCAGCCATCCAGTG
MetThrArgMetProAsnLeuMetGlyHisGluAsnGlnArgGluAlaAlaIleGlnLeu

670

690

710

CACGAGTTCGCGCCGCTGGTGGAGTACGGCTGCCACGCCACCTCCGCTTCTCCTGTGC
HisGluPheAlaProLeuValGluTyrGlyCysHisGlyHisLeuArgPhePheLeuCys

730

750

770

TCGCTGTACGCGCCGATGTGCACCGAGCAGGTCTCTACCCCCATCCCCGCCTGCCGGTC
SerLeuTyrAlaProMetCysThrGluGlnValSerThrProIleProAlaCysArgVal

790

810

830

ATGTGCGAGCAGGCCCGGCTCAAGTGCTCCCCATTATGGAGCAGTTCAACTTCAAGTGG
MetCysGluGlnAlaArgLeuLysCysSerProIleMetGluGlnPheAsnPheLysTrp

850

870

890

CCCGACTCCCTGGACTGCCGGAAACTCCCCAACAAAGAACGACCCAACTACCTGTGCATG
ProAspSerLeuAspCysArgLysLeuProAsnLysAsnAspProAsnTyrLeuCysMet

910

930

950

GAGGCGCCAACAACGGCTCGGACGAGCCCACCCGGGGCTCGGGCCTGTTCCGCCGCTG
GluAlaProAsnAsnGlySerAspGluProThrArgGlySerGlyLeuPheProProLeu

970

990

1010

TTCCGGCCGCAGCGGCCACAGCGCGCAGGAGCACCGCTGAAGGACGGGGCCCGGG
PheArgProGlnArgProHisSerAlaGlnGluHisProLeuLysAspGlyGlyProGly

1030

1050

1070

CGCGCGGCTGCGACAACCCGGCAAGTTCCACCACGTGGAGAAGAGCGCGTCGTGCGCG
ArgGlyGlyCysAspAsnProGlyLysPheHisHisValGluLysSerAlaSerCysAla

1090

1110

1130

CCGCTCTGCACGCCGGCGTGGACGTGTACTGGAGCCGCGAGGACAAGCGCTTCGAGTG
ProLeuCysThrProGlyValAspValTyrTrpSerArgGluAspLysArgPheAlaVal

1150

1170

1190

GTCTGGCTGCCATCTGGCGGTGCTGTGCTTCTCCAGCGCCTCACCGTGCTCACC
ValTrpLeuAlaIleTrpAlaValLeuCysPhePheSerSerAlaPheThrValLeuThr

1210

1230

1250

TTCCTCATCGACCCGGCCGCTCCGCTACCCGAGCGCCCCATCATCTCCTCTCCATG
PheLeuIleAspProAlaArgPheArgTyrProGluArgProIleIlePheLeuSerMet

1270

1290

1310

TGCTACTGCGTCTACTCCGTGGGCTACCTCATCCGCCTCTGCCGGCGCCGAGAGCATC
CysTyrCysValTyrSerValGlyTyrLeuIleArgLeuPheAlaGlyAlaGluSerIle

1330

1350

1370

GCCTGCGACCGGGACAGCGGCCAGCTCTATGTCATCCAGGAGGGACTGGAGAGCACCGGC
AlaCysAspArgAspSerGlyGlnLeuTyrValIleGlnGluGlyLeuGluSerThrGly

1390

1410

1430

TGCACGCTGGTCTCCTGGCCTCTACTACTTCGGCATGGCCAGCTCGCTGTGGTGGTG
CysThrLeuValPheLeuValLeuTyrTyrPheGlyMetAlaSerSerLeuTrpTrpVal

1450

1470

1490

GTCCTCACGCTCACCTGGTTCTGGCCGCCGGCAAGAAGTGGGCCACGAGGCCATCGAA
ValLeuThrLeuThrTrpPheLeuAlaAlaGlyLysLysTrpGlyHisGluAlaIleGlu

1510

1530

1550

GCCAACAGCAGCTACTTCCACCTGGCAGCCTGGCCATCCGGCGGTGAAGACCATTCTG
AlaAsnSerSerTyrPheHisLeuAlaAlaTrpAlaIleProAlaValLysThrIleLeu

1570

1590

1610

ATCCTGGTCATGCGCAGGGTGGCGGGGACGAGCTCACCGGGCTGCTACGTGGCAGC
IleLeuValMetArgArgValAlaGlyAspGluLeuThrGlyValCysTyrValGlySer

1630

1650

1670

ATGGACGTCAACGCGCTCACCGGCTTCGTGCTCATTCCCTGGCCTGCTACCTGGTCATC
MetAspValAsnAlaLeuThrGlyPheValLeuIleProLeuAlaCysTyrLeuValIle

1690

1710

1730

FIG. 9C

GGCACGTCTCATCCTCTCGGGCTTGTGGCCCTGTTCCACATCCGGAGGGTGATGAAG
GlyThrSerPheIleLeuSerGlyPheValAlaLeuPheHisIleArgArgValMetLys

1750

1770

1790

ACGGGCGGCAGAACACGGACAAGCTGGAGAAGCTCATGGTGCATCGGGCTTTCTCT
ThrGlyGlyGluAsnThrAspLysLeuGluLysLeuMetValArgIleGlyLeuPheSer

1810

1830

1850

G TGCTGTACACCGTGCCGCCACCTGTGTGATGCCCTGCTACTTTACGAACGCCTCAAC
ValLeuTyrThrValProAlaThrCysValIleAlaCysTyrPheTyrGluArgLeuAsn

1870

1890

1910

ATGGATTACTGGAAGATCCTGGCGGCCAGCACAAAGTGC AAAATGAACAAACCAGACTAAA
MetAspTyrTrpLysIleLeuAlaAlaGlnHisLysCysLysMetAsnAsnGlnThrLys

1930

1950

1970

ACGCTGGACTGCCTGATGCCGCCCTCCATCCCCGCCGTGGAGATCTTCATGGTGAAGATC
ThrLeuAspCysLeuMetAlaAlaSerIleProAlaValGluIlePheMetValLysIle

1990

2010

2030

TTTATGCTGGTGGTGGGGATCACCAAGCGGGATGTGGATTGGACCTCCAAGACTCTG
PheMetLeuLeuValValGlyIleThrSerGlyMetTrpIleTrpThrSerLysThrLeu

2050

2070

2090

CAGTCCTGGCAGCAGGTGTGCAGCCGTAGGTTAAAGAAGAAGAGCCGGAGAAAACCGGCC
GlnSerTrpGlnGlnValCysSerArgArgLeuLysLysSerArgArgLysProAla

2110

2130

2150

AGCGTGATCACCAAGCGGTGGGATTACAAAAAAAGCCCAGCATCCCCAGAAAACCTACCCAC
SerValIleThrSerGlyGlyIleTyrLysLysAlaGlnHisProGlnLysThrHisHis

2170

2190

2210

GGGAAATATGAGATCCCTGCCAGTCGCCACCTGCGTGTGAACAGGGCTGGAGGGAGG
GlyLysTyrGluIleProAlaGlnSerProThrCysValEnd

2230

2250

2270

FIG. 9D

GCACAGGGCGCCCGAGCTAAGATGTGGGCTTTCTTGGTGTAAAACTTCTTCT

2290

2310

2330

TCTTCTTTTTTTTTTATAAAAGCAAAAGAGAAATACATAAAAAAGTGTACCTG

2350

2370

2390

AAATTCAAGGATGCTGTGATACTGAAAGGAAAATGTACTTAAAGGGTTTGTGTT

2410

2430

2450

TTGGTTTCCAGCGAAGGGAAGCTCCTCCAGTGAAGTAGCCTTTGTGTAACATTG

2470

2490

2510

GGTAAAGTAGTTGATTCAGCCCTCAGAAGAAAACTTTGTAGAGCCCTCCSTAAAT

2530

2550

2570

ACATCTGTGTATTGAGTTGGCTTGCTACCCATTACAAATAAGAGGACAGATAACTGC

2590

2610

2630

TTTCAAATTCAAGAGCCTCCCTGGGTTAACAAATGAGCCATCCCCAGGGCCCACCCCC

2650

2670

2690

AGGAAGGCCACAGTGCTGGCGGCATCCCTGCAGAGGAAAGACAGGGACCCGGGCCGCC

2710

2730

2750

TCACACCCAGTGGATTGGAGTTGCTTAAAGACTCCGGCCTTCACCAATAGTCTCT

2770

2790

2810

CTGCAAGACAGAAACCTCCATCAAACCTCACATTGTGAACCAAACGATGTGCAATACA

2830

2850

2870

TTTTTTCTTTCTTGTAAAATAAAAGAGAAACAAGTATTTGCTATATATAAGACA

2890

2910

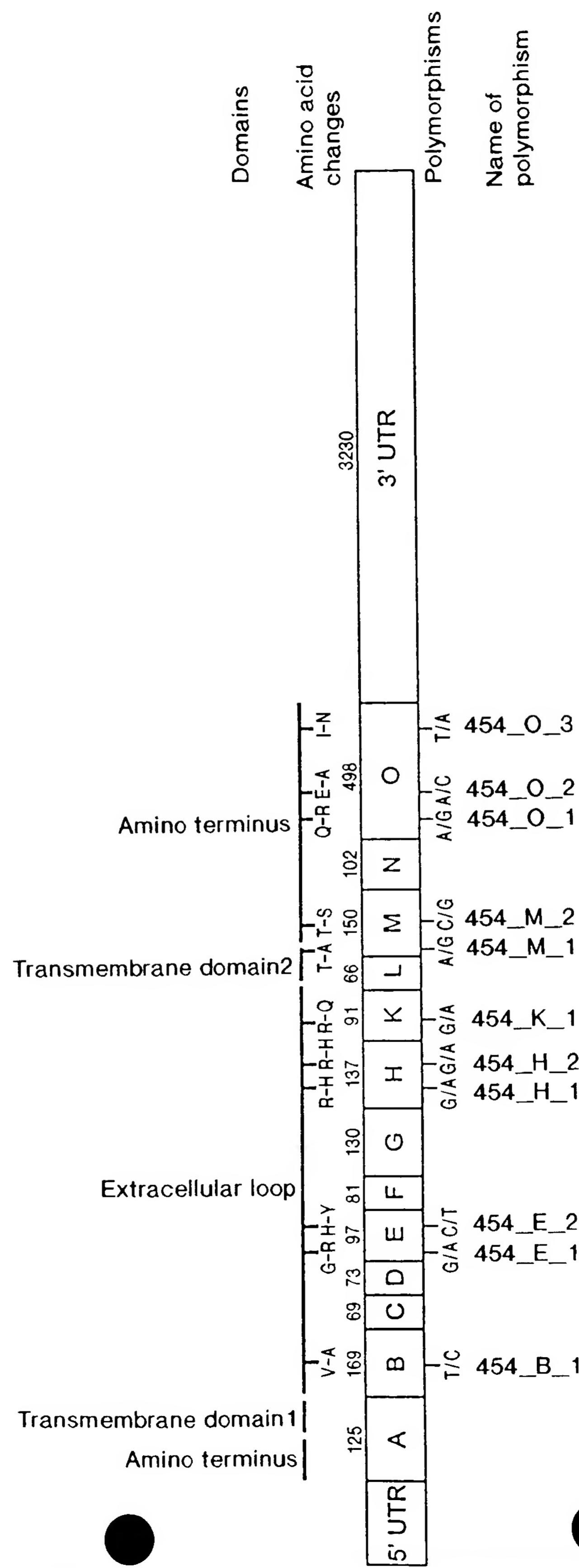
2930

FIG. 9E

ACAAAAGAAATCTCCTAACAAAAGAACTAAGAGGCCAGCCCTCAGAAACCCTTCAGTGC
2950 2970 2990
TACATTTGTGGCTTTAATGGAAACCAAGCCAATGTTAGACGTTGGACTGATTG
3010 3030 3050
TGGAAAGGAGGGGGGAAGAGGGAGAAGGATCATTCAAAAGTTACCAAAGGGCTTATTGA
3070 3090 3110
CTCTTCTATTGTTAACAAATGATTCCACAAACAGATCAGGAAGCACTAGGTTGGCAG
3130 3150 3170
AGACACTTGTCTAGTGTATTCTCTCACAGTGCCAGGAAAGAGTGGTTCTGCGTGTGT
3190 3210 3230
ATATTTGTAATATGATATTTCATGCTCCACTATTTATTAAAAATAAAATATGTTCA
3250
TTTAGTTGCTGCT

FIG. 9F

FIG. 10



Chr. 12 Case(Asthma)/Control: Alleles

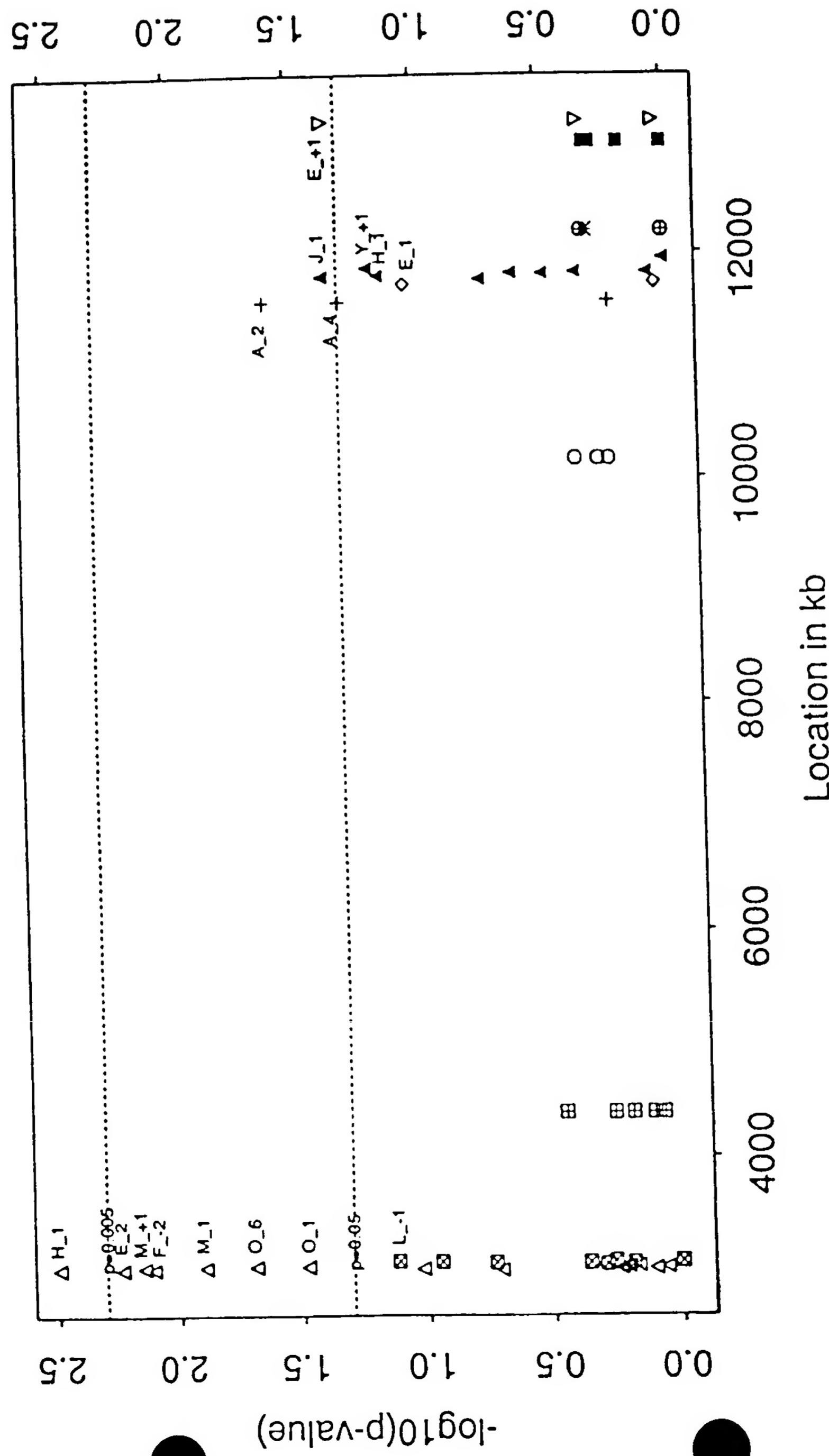


FIG. 11

Chr. 12 Case(Asthma)/Control: Alleles

US

UK

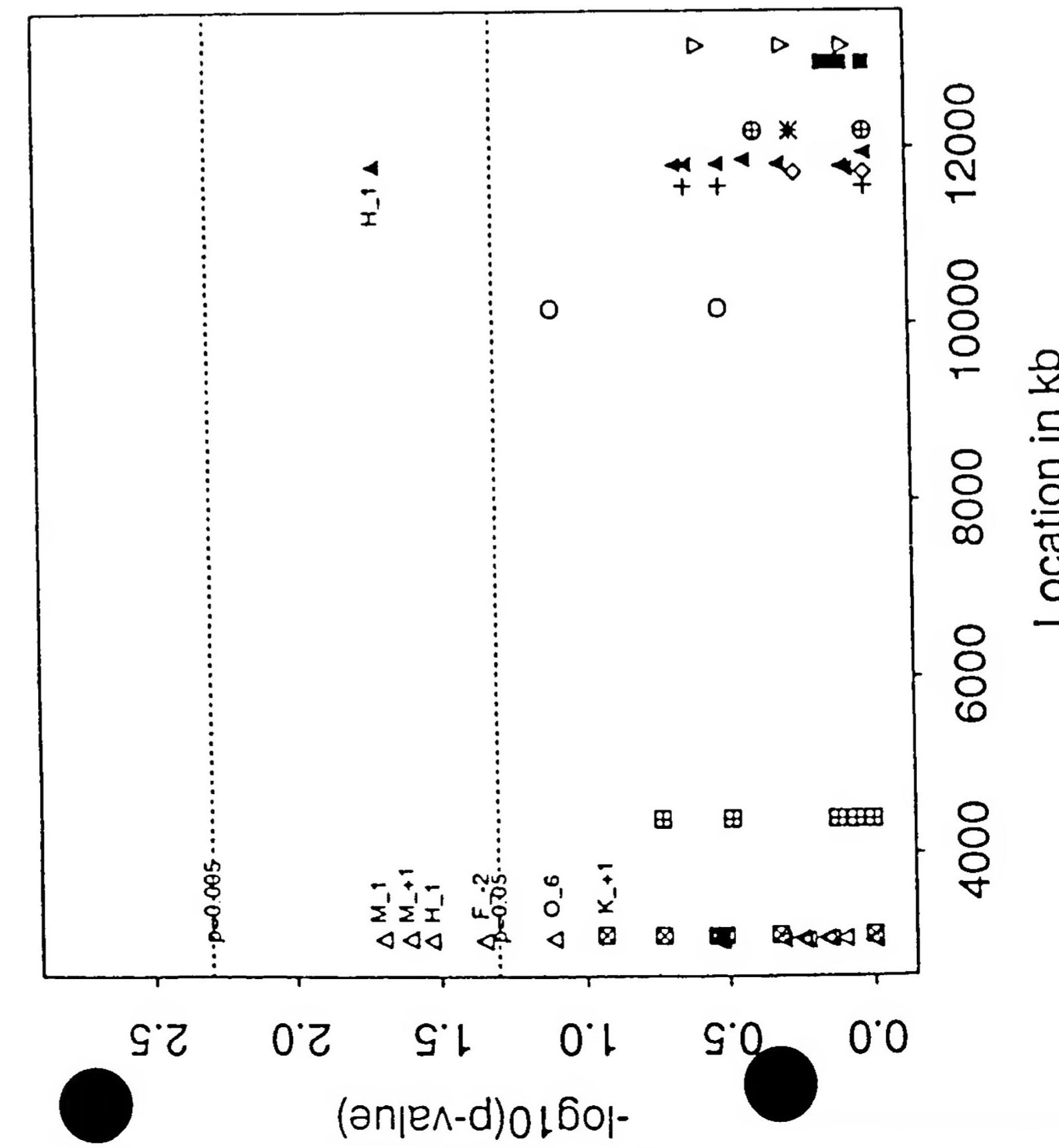


FIG. 12

Chr. 12 Case(BH R (PC20 <= 16 mg/ml) & Asthma)/Control: Alleles

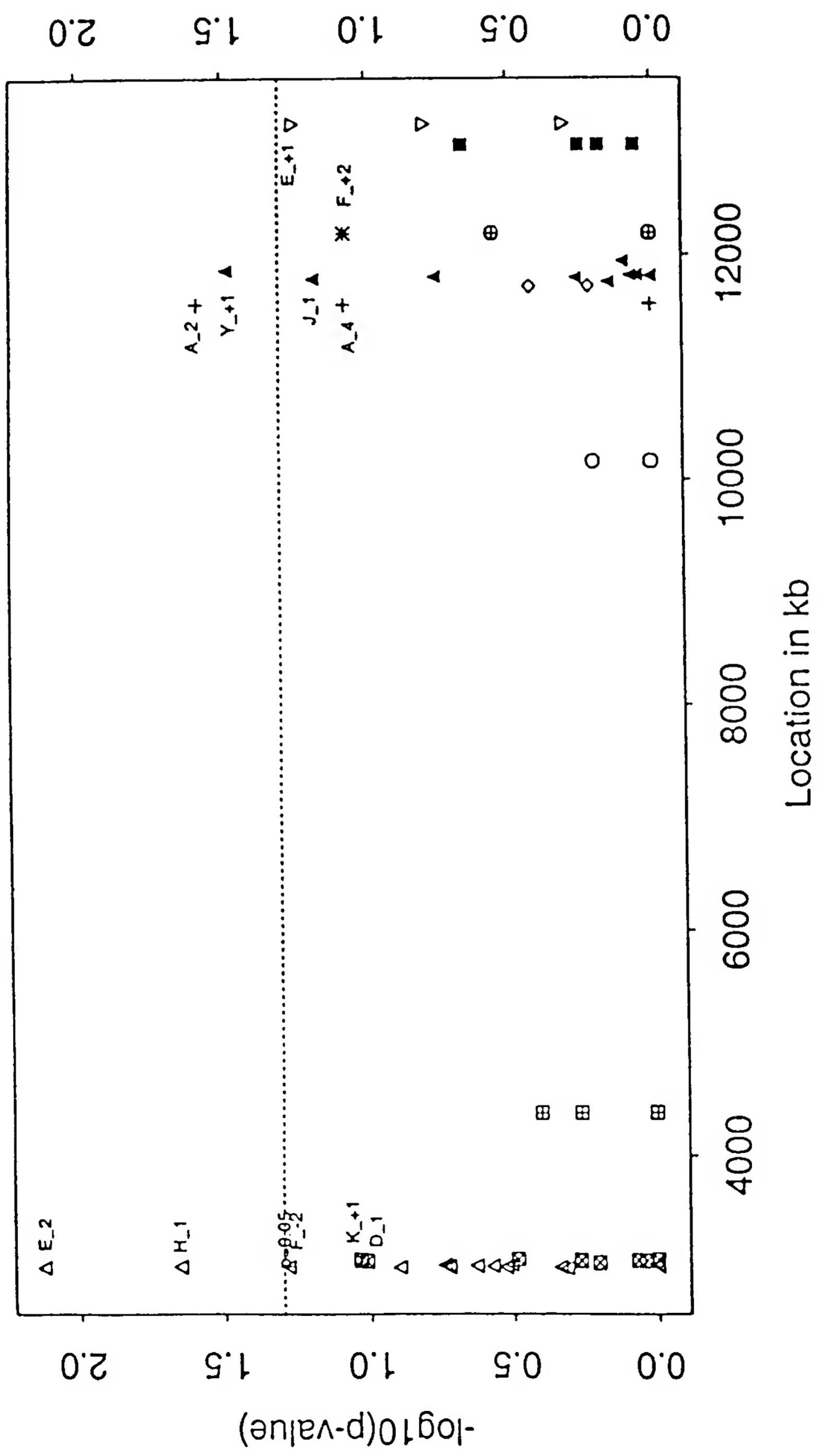


Diagram illustrating the locations of various genes along a linear scale:

- Gene 454
- Gene 436
- Gene 515
- Gene 570
- Gene 561
- Gene 581
- Gene 698
- Gene 722
- Gene 757
- Gene 722
- Gene 702
- Gene 214

Legend:

- Gene 454
- △ Gene 436
- ⊗ Gene 515
- Gene 570
- ▲ Gene 561
- ◇ Gene 581
- ◊ Gene 698
- ◆ Gene 722
- ▽ Gene 757
- ◆ Gene 722
- Gene 702
- ▽ Gene 214

FIG. 13

Chr. 12 Case(BHR (PC20 \leq 16 mg/ml) & Asthma)/Control: Alleles

US UK

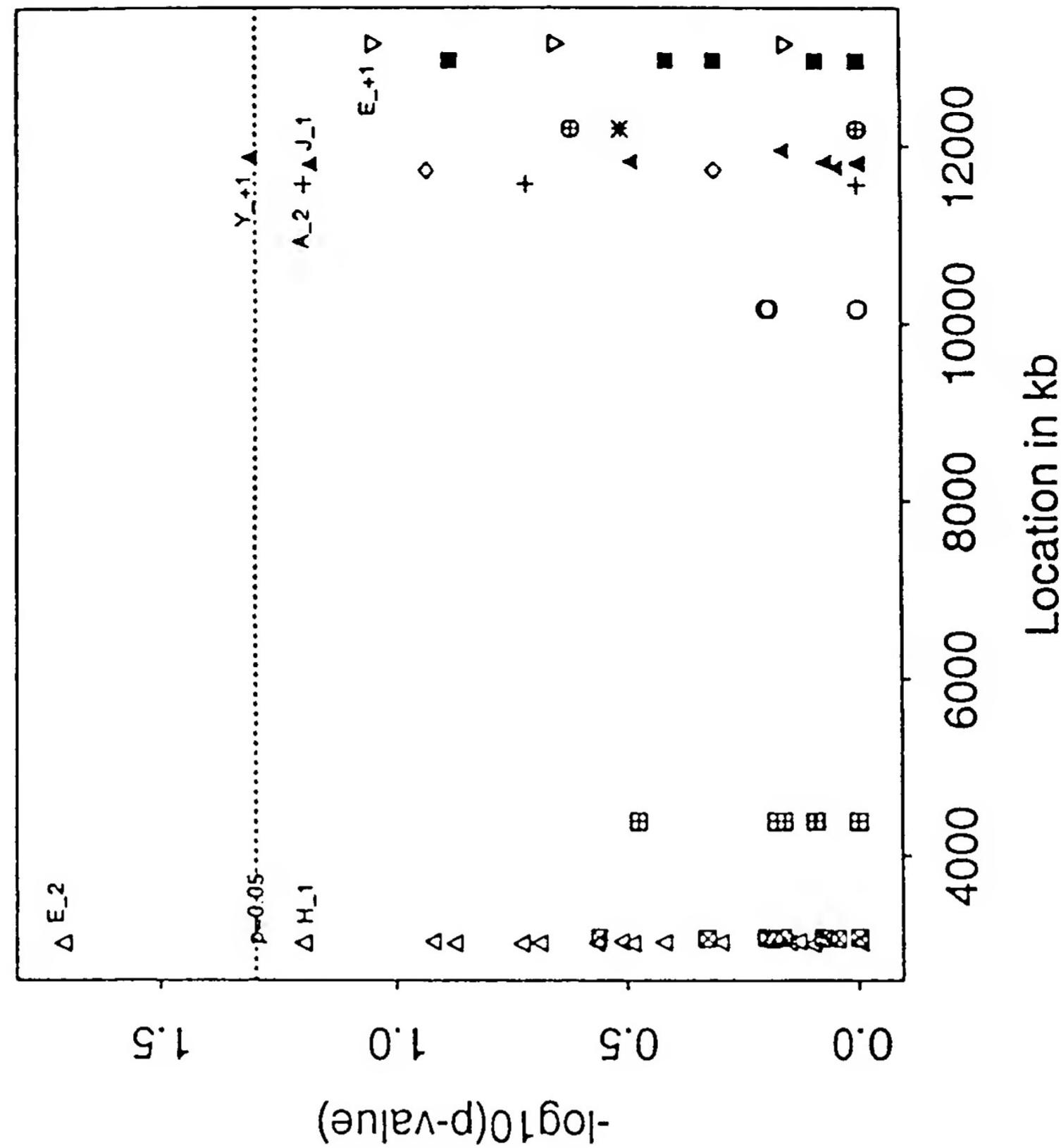
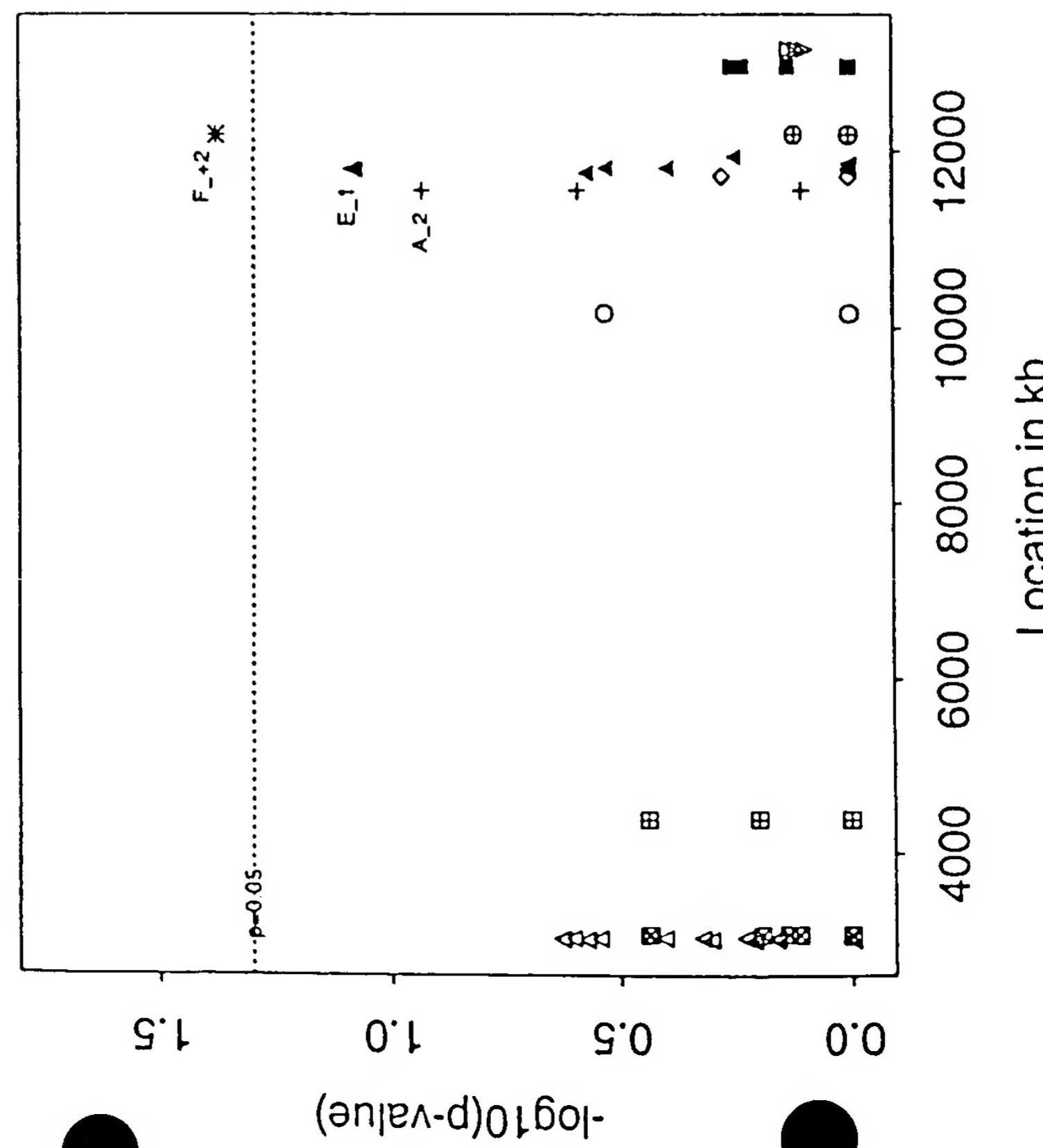
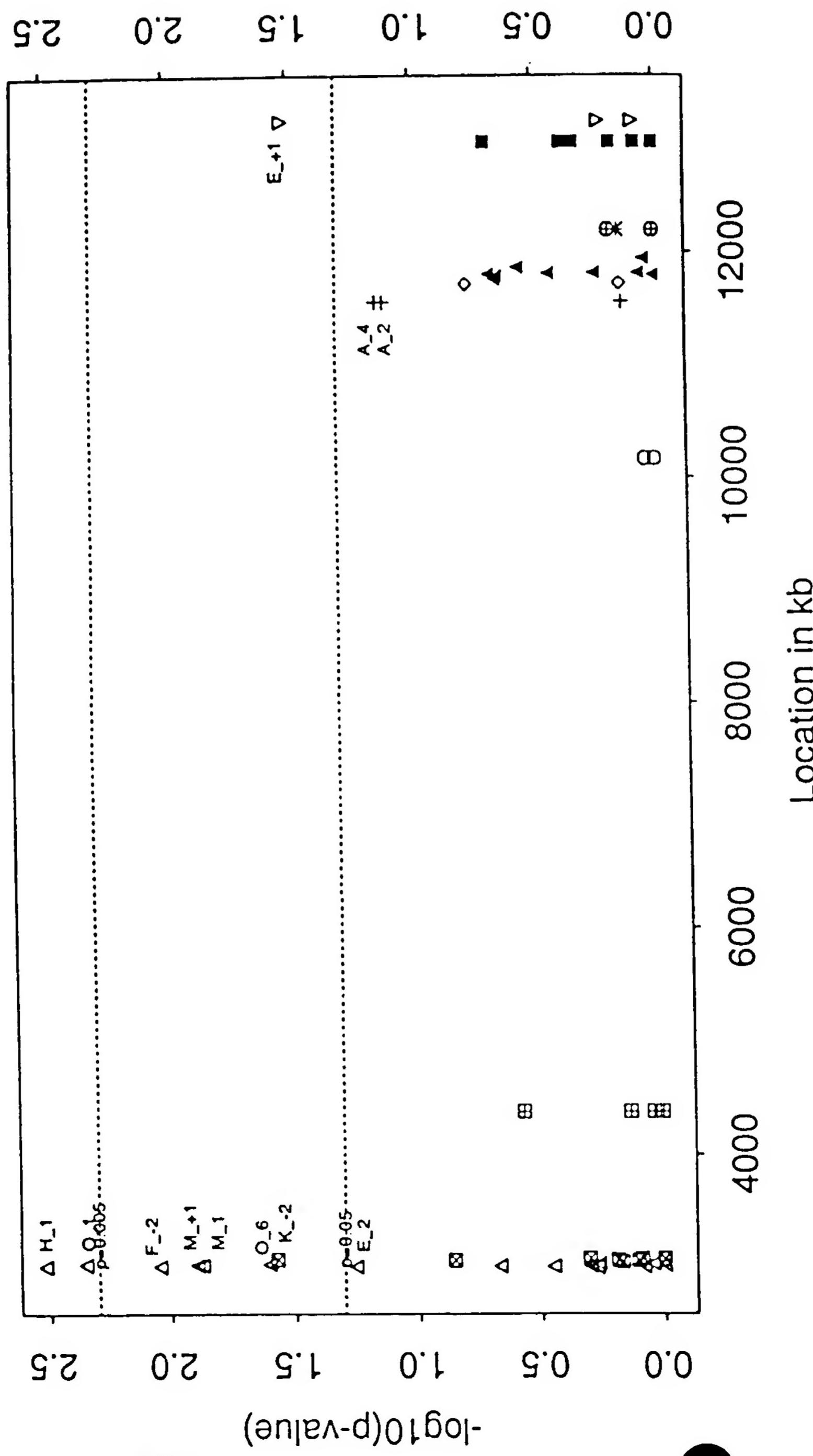


FIG. 14

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles



Legend for the map:

- gene 454: open triangle
- gene 436: open circle
- gene 515: plus sign (+)
- gene 570: open diamond
- gene 698: open square
- gene 722: open circle with cross
- gene 561: open triangle with dot
- gene 581: open circle with dot
- gene 702: solid square
- gene 724: open triangle with dot

FIG. 15

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

US UK

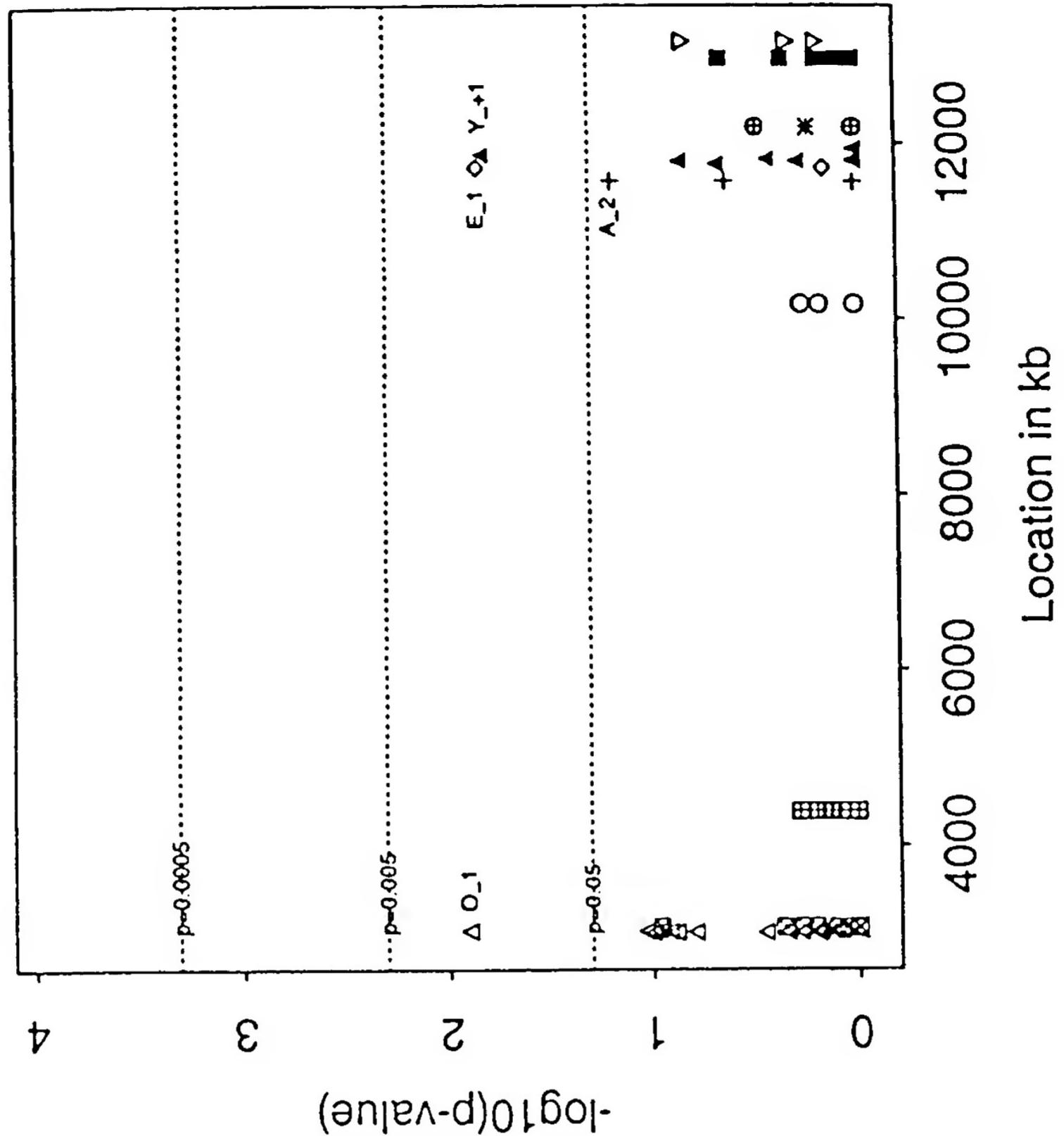
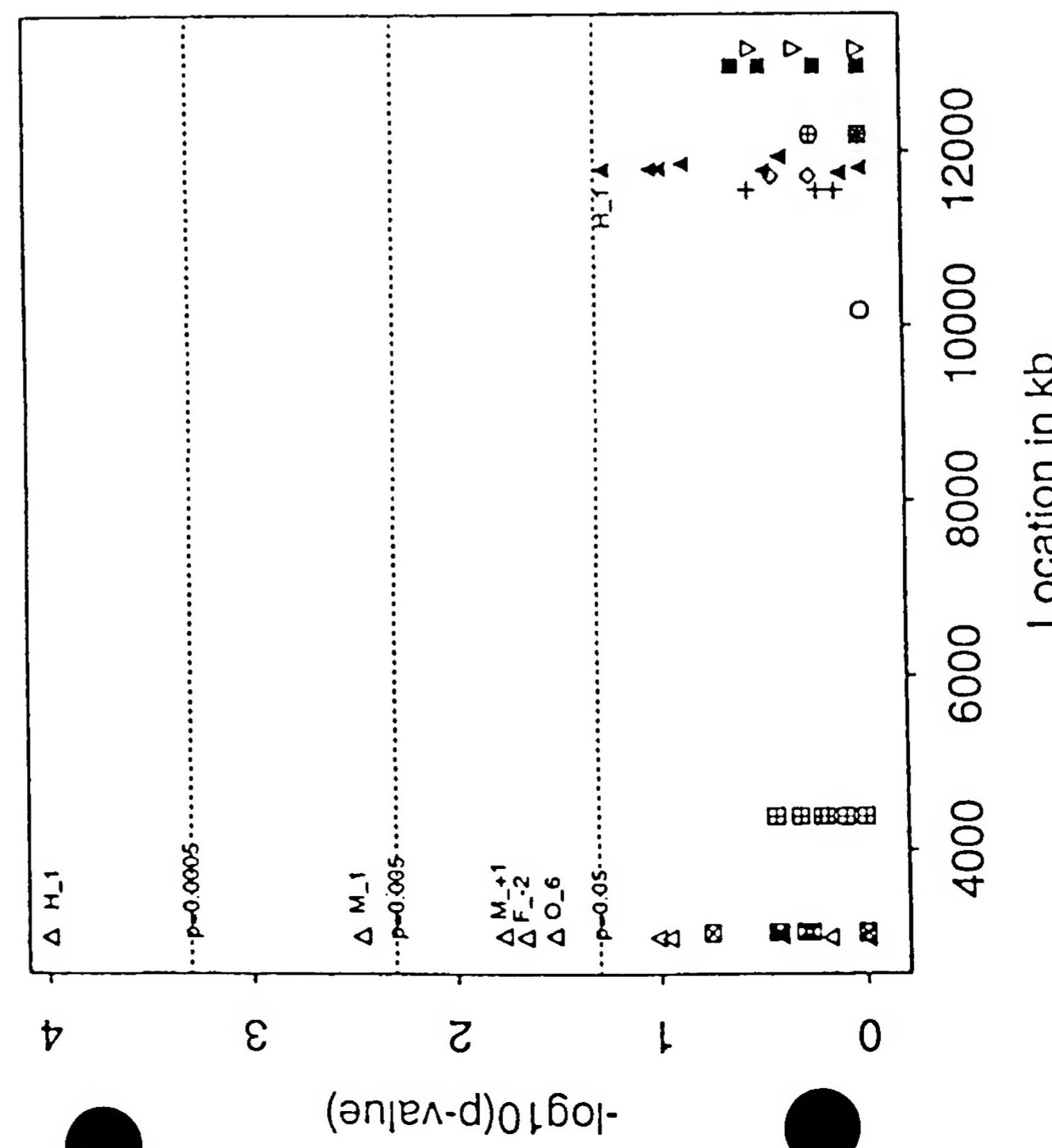


FIG. 16

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

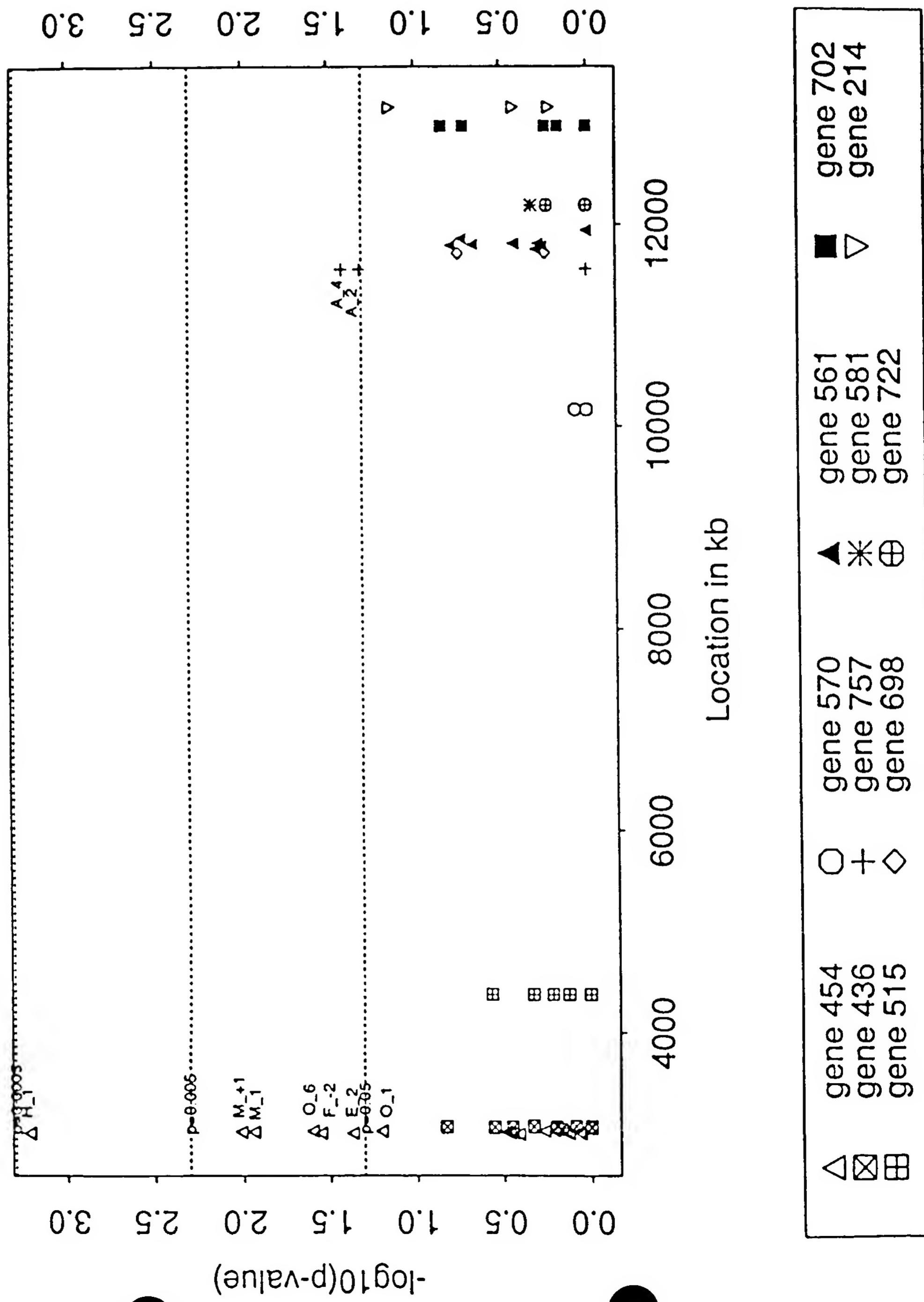


FIG. 17

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

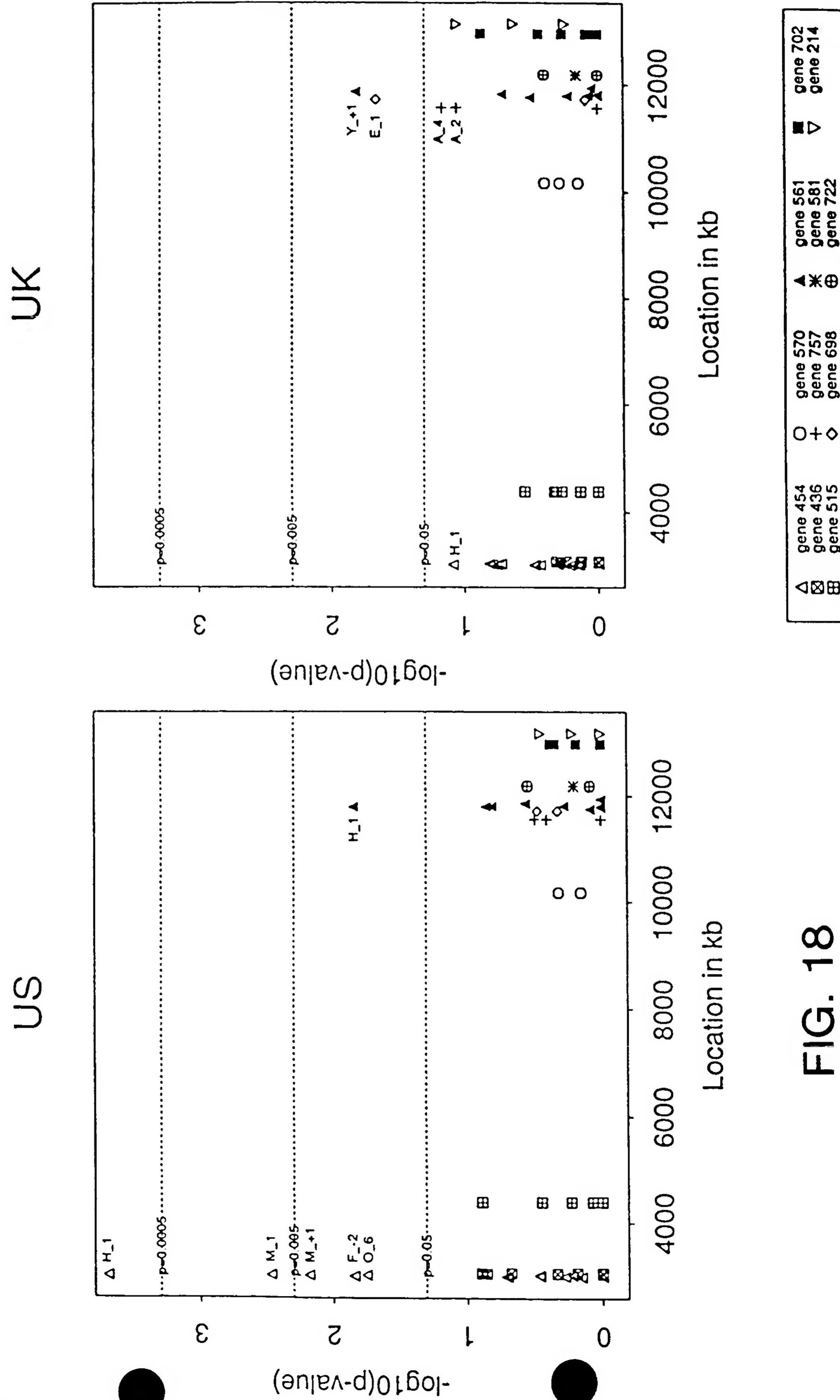


FIG. 18

Chr. 12 Case(Asthma)/Control: Haplotype

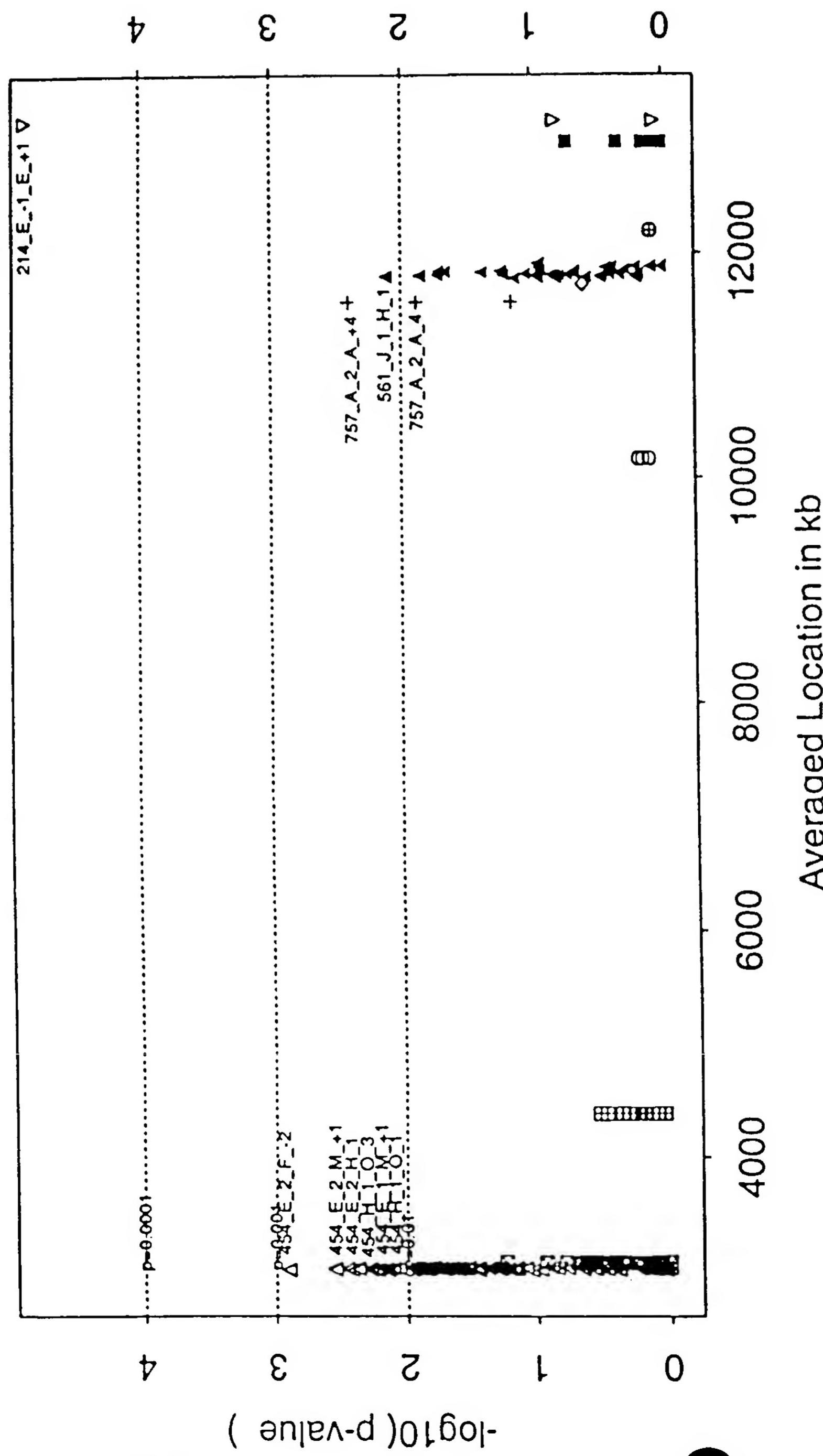


FIG. 19

Chr. 12 Case(Asthma)/Control: Haplotype

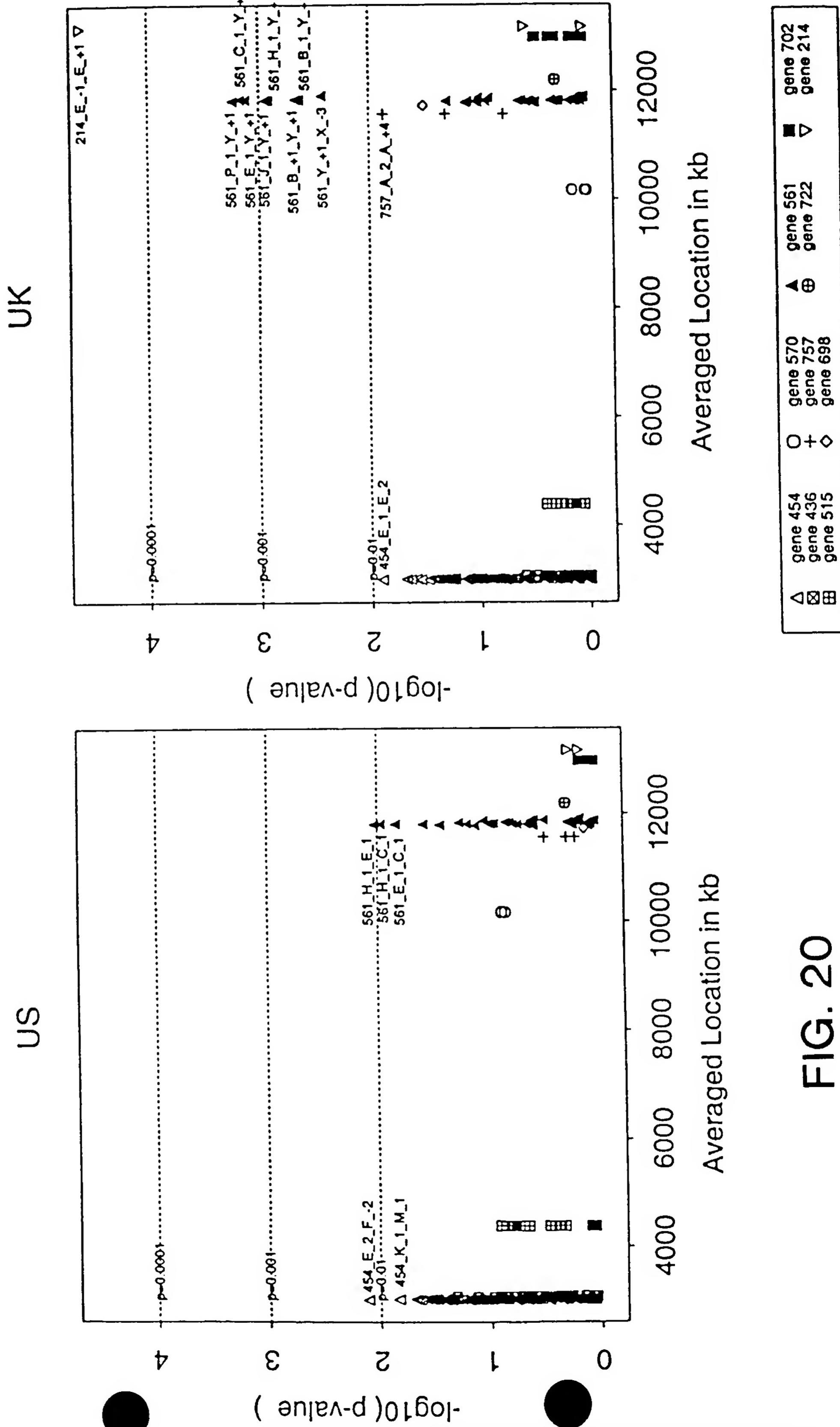


FIG. 20

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

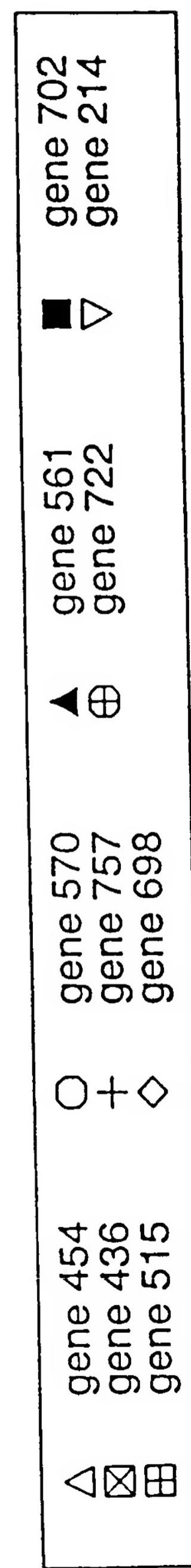
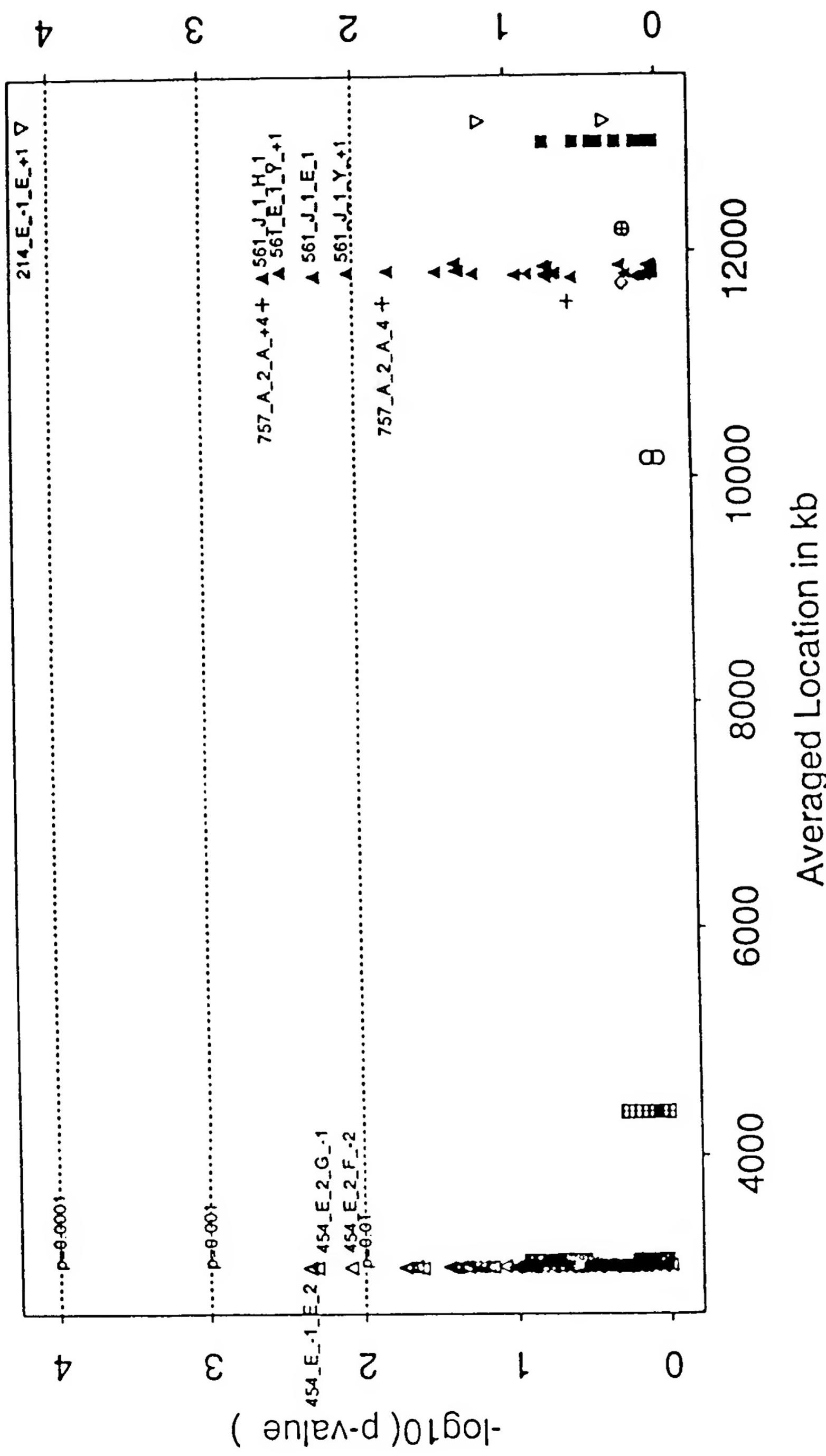
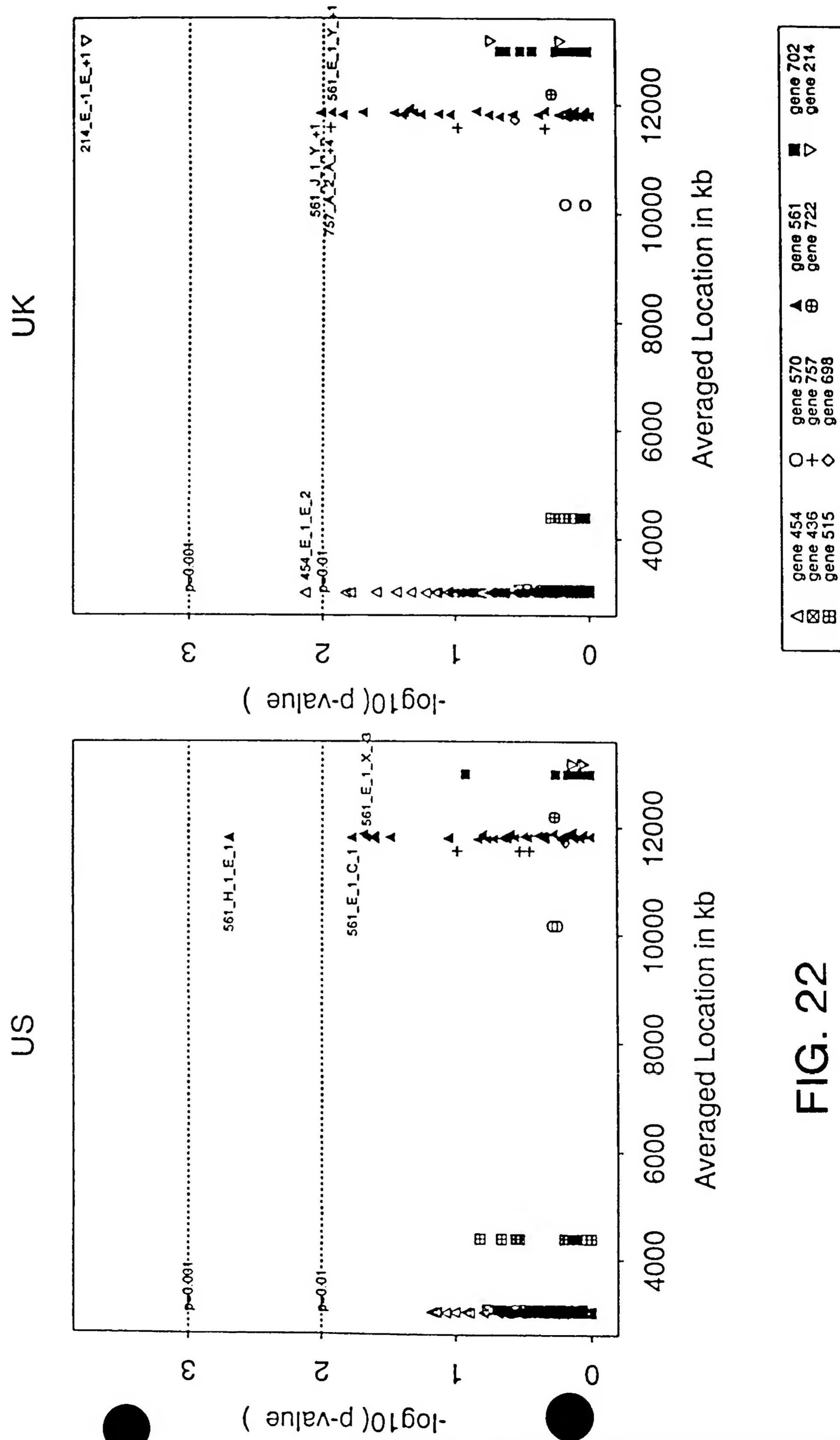


FIG. 21

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype



Chr. 12 Case(Total IgE & Asthma)/(Control: Haplotype

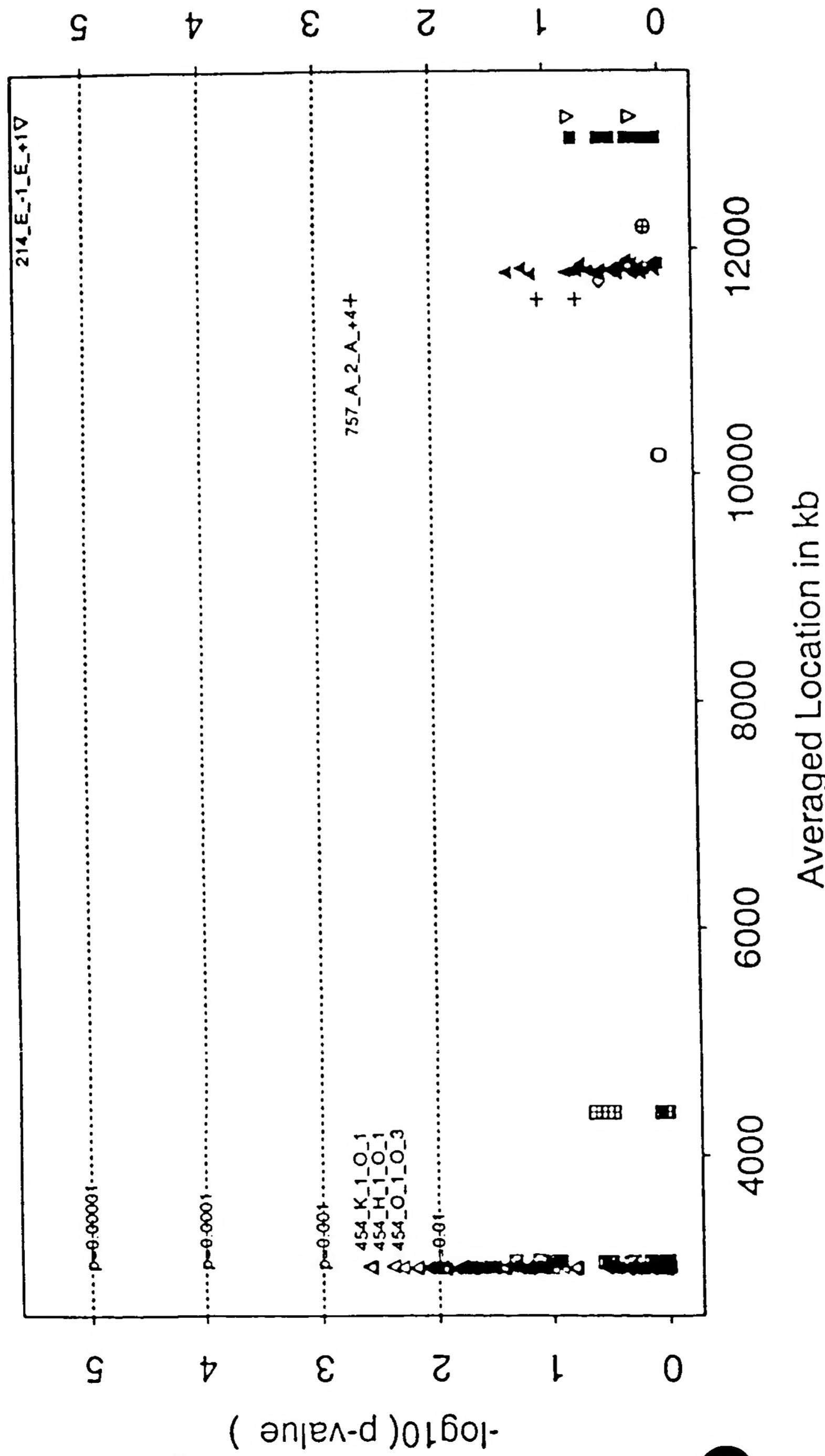


FIG. 23

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

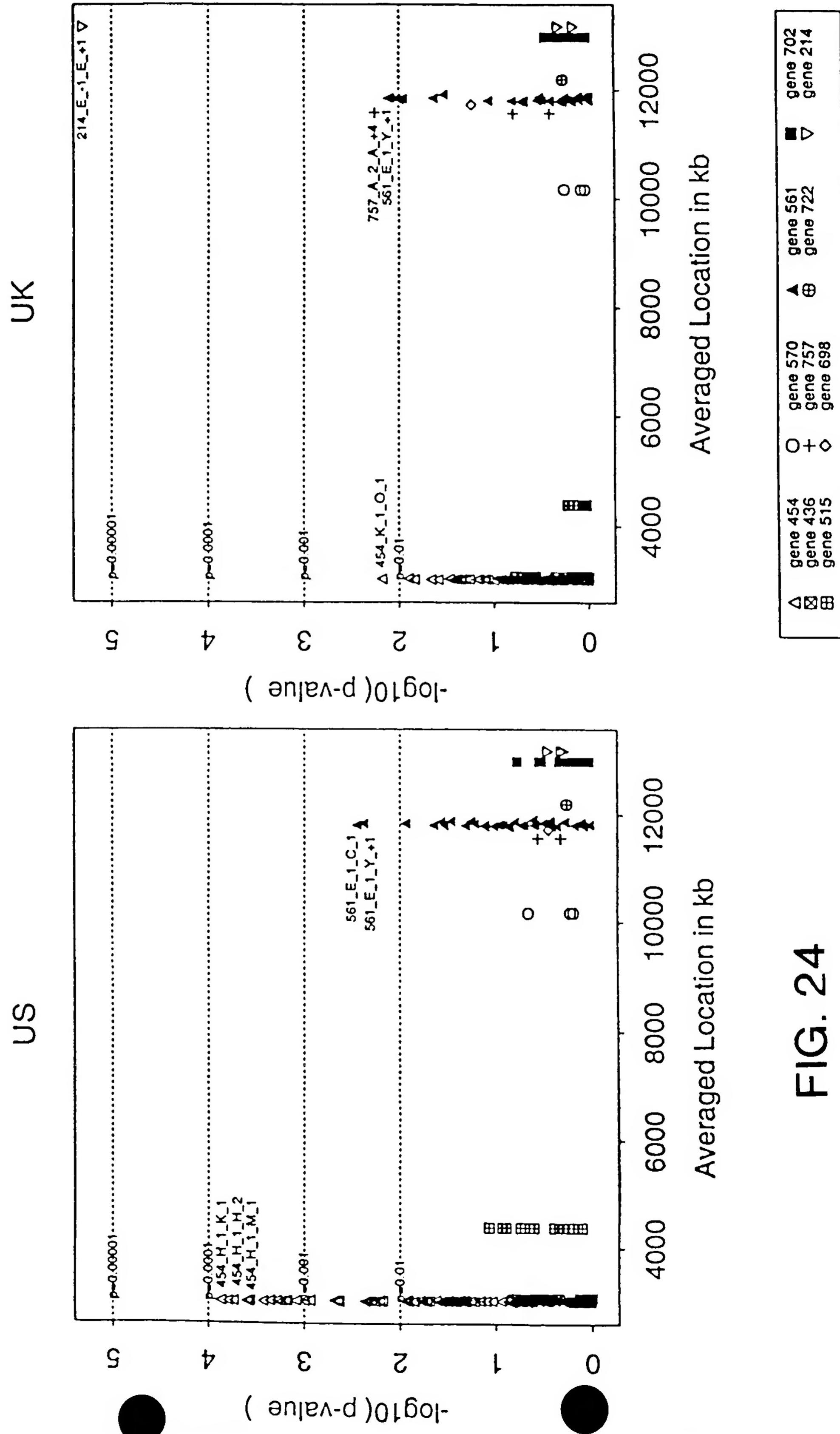


FIG. 24

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

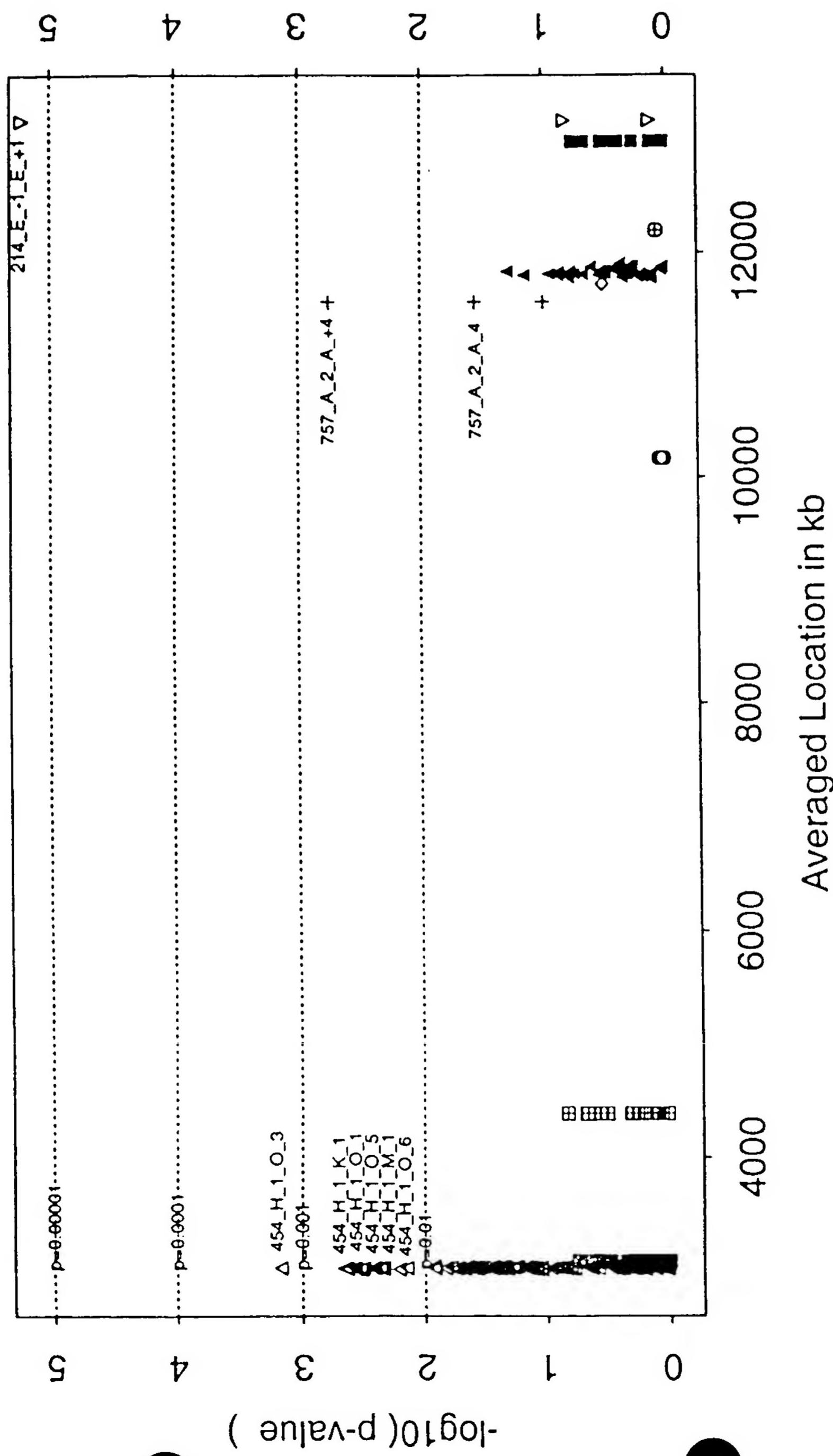


FIG. 25

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

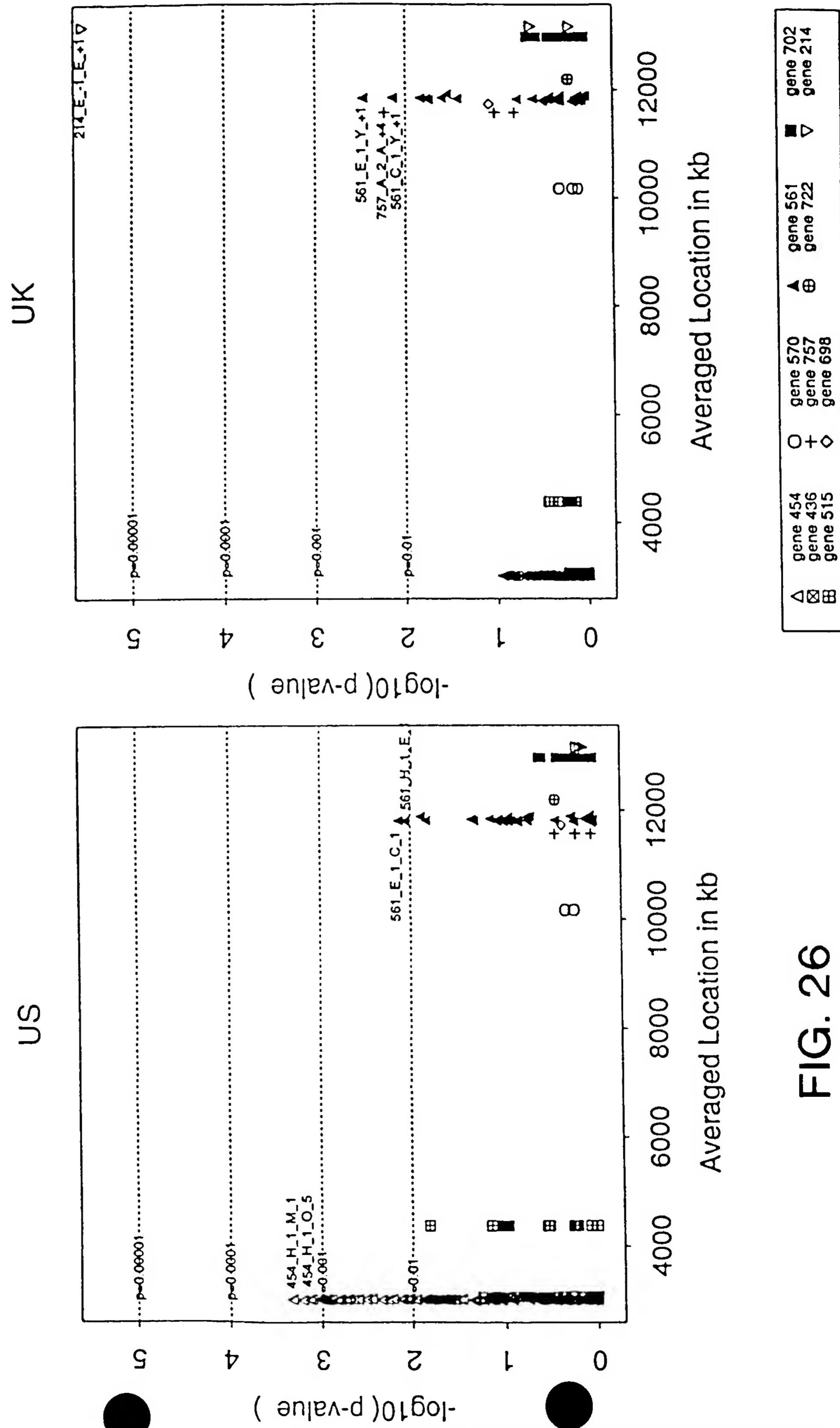


FIG. 26

10 30 50
CTTGGAAATGACCCGCCACACCTGAAGCCTGCAGGTGCTGAGGCCACATTGATCAGACC

70 90 110
CAAGCTTGGGAGACCGCTGGGAAATTCCTCTCCTGAGACCAGGAACTCAG

130 150 170
CAGAGAAACTTGAAATGAAGGATGCCACCCAGGGAGAGTATCTCCTGAGA

190 210 230
TCCCCATCATGCAGGCCTTCCCACAAGGGCCCGGCAGCATGACAAGGTGAAGGCAGAGTAT

250 270 290
GTGCATCTCAACCAYCCGCTCACCTCGTGACCAGAGAGCGCGATTGGCCGTGAAGGAG

310 330 350
AAACACCAGCTCCAAGCCAAGCTGGAGAACCTAGAACAGGTCTGAAGCATATGCGAGAG
MetArgGlu

370 390 410
GCGGCTGAACGGCGGCAGCAGCTGCAGTTGGAGCATGACCAGGCCCTGGCTGTTCTCAGT
AlaAlaGluArgArgGlnGlnLeuGlnLeuGluHisAspGlnAlaLeuAlaValLeuSer

430 450 470
GCCAAGCAGCAGGAAATTGACCTCTGCAGAAGTCCAAGGTTGAGAGCTGGAAGAGAAA
AlaLysGlnGlnGluIleAspLeuLeuGlnLysSerLysValArgGluLeuGluLys

490 510 530
TGCCGGACTCAAAGTGAGCAGTTCAACCTGCTGTCCCGGGACCTGGAGAAGTTCCGGCAG
CysArgThrGlnSerGluGlnPheAsnLeuLeuSerArgAspLeuGluLysPheArgGln

550 570 590
CACGCTGGCAAGATTGACCTGCTGGTGGCAGCGCGGTGGCCCCCTGGACATCTCCACG
HisAlaGlyLysIleAspLeuLeuGlyGlySerAlaValAlaProLeuAspIleSerThr

FIG. 27A

610 630 650
GCCCCCAGCAAGCCTTCCCACAGTCATGAATGGCCTAGCCACCTCCCTCGGCAAAGGT
AlaProSerLysProPheProGlnPheMetAsnGlyLeuAlaThrSerLeuGlyLysGly

670 690 710
CAGGAGAGCGCTATTGGAGGCAGCTCTGCGATCGGTGAATATATCCGGCCCTTCCGCAG
GlnGluSerAlaIleGlyGlySerSerAlaIleGlyGluTyrIleArgProLeuProGln

730 750 770
CCTGGTGACAGGCCGGAGCCTCTGTCCGCCAAGCCCACCTCCTGTCGAGATCCGGTAGC
ProGlyAspArgProGluProLeuSerAlaLysProThrPheLeuSerArgSerGlySer

790 810 830
GCAAGATGCAGATCTGAGTCAGACATGGAGAATGAACGGAATTCCAATACTCCAAGCAG
AlaArgCysArgSerGluSerAspMetGluAsnGluArgAsnSerAsnThrSerLysGln

850 870 890
AGATACTGGGAAAGGTCCACCTCTGTGTGCCCGCTATAAGTTACAACCCCTTCGATGGA
ArgTyrSerGlyLysValHisLeuCysValAlaArgTyrSerTyrAsnProPheAspGly

910 930 950
CCGAACGAGAACCCCGAAGCTGAGCTGCCCTCACGGCGGGAAAATACCTCTACGTCTAT
ProAsnGluAsnProGluAlaGluLeuProLeuThrAlaGlyLysTyrLeuTyrValTyr

970 990 1010
GGAGACATGGATGAGGATGGGTTCTATGAAGGAGAGCTCCTCGATGCCAGAGGGCTG
GlyAspMetAspGluAspGlyPheTyrGluGlyGluLeuLeuAspGlyGlnArgGlyLeu

1030 1050 1070
GTGCCCTCCAACCTCGTGGACTTGTGCAGGACAACGAGTCGCGGTTGGCAAGCACGCTG
ValProSerAsnPheValAspPheValGlnAspAsnGluSerArgLeuAlaSerThrLeu

1090 1110 1130
GGGAACGAGCAGGATCAGAACTTCATCAACCATTCCGGCATCGGCCTGGAGGGAGAGCAC
GlyAsnGluGlnAspGlnAsnPheIleAsnHisSerGlyIleGlyLeuGluGlyGluHis

1150 1170 1190
ATCCTGGACCTCCACTCCCCAACCCACATAGATGCCGGCATCACCGACAAACAGTGCCGGG

IleLeuAspLeuHisSerProThrHisIleAspAlaGlyIleThrAspAsnSerAlaGly

1210 1230 1250
ACCTGGACGTGAACATCGACGACATCGGAGAAGACATCGTGCCTTACCCCTAGAAAAATC
ThrLeuAspValAsnIleAspAspIleGlyGluAspIleValProTyrProArgLysIle

1270 1290 1310
ACCTCATCAAACAACCGCCAAAAGTGTATTGTGGCTGGAGCCCCCGGCGGTGCCA
ThrLeuIleLysGlnLeuAlaLysSerValIleValGlyTrpGluProProAlaValPro

1330 1350 1370
CCAGGATGGGAACGGTGAGCAGCTACAACTGGCCTGGTGGACAAGGAGACACGCATGAAC
ProGlyTrpGlyThrValSerSerTyrAsnValLeuValAspLysGluThrArgMetAsn

1390 1410 1430
CTCACGCTGGGAGCAGAACTAAAGCCCTATCGAGAAGCTAACATGGCAGCCTGCACC
LeuThrLeuGlySerArgThrLysAlaLeuIleGluLysLeuAsnMetAlaAlaCysThr

1450 1470 1490
TACCGCATCTCCGTGCAGTGCCTCACAGCAGGGCAGCTGGATGAGCTGCAGTGCACG
TyrArgIleSerValGlnCysValThrSerArgGlySerSerAspGluLeuGlnCysThr

1510 1530 1550
CTGCTGGTGGCAAGGACGTGGTGGCCCTCCCACCTGCGGGTGGACAACATCACG
LeuLeuValGlyLysAspValValAlaProSerHisLeuArgValAspAsnIleThr

1570 1590 1610
CAGATCTCCGCCAGCTCTCCTGGCTACCCACCAACAGCAACTACAGCCACGTCACTTC
GlnIleSerAlaGlnLeuSerTrpLeuProThrAsnSerAsnTyrSerHisValIlePhe

1630 1650 1670
CTCAACGAGGAGGAGTTGCACATCGTCAAGGCCGCCAGGTACAAGTACCAAGTTCTCAAT
LeuAsnGluGluGluPheAspIleValLysAlaAlaArgTyrLysTyrGlnPhePheAsn

1690 1710 1730
CTCAGGCCAACATGGCCTATAAGGTGAAGGTTCTGGCAAACCCACCAGATGCCGTGG
LeuArgProAsnMetAlaTyrLysValLysValLeuAlaLysProHisGlnMetProTrp

1750

1770

1790

CAGCTCCGCTGGAGCAAAGGGAGAAGAAGGAGGCCTTGTGGAGTTCTCCACGTTGCC
 GlnLeuProLeuGluGlnArgGluLysLysGluAlaPheValGluPheSerThrLeuPro

1810

1830

1850

GCAGGACCCCCAGCACCCCCACAAGATGTTACCGTCCAGGCTGGGTGACCCCCGCCACC
 AlaGlyProProAlaProProGlnAspValThrValGlnAlaGlyValThrProAlaThr

1870

1890

1910

ATCCGGGTCTCCTGGAGACCACCTGTGCTGACGCCACCGGGCTGTCCAATGGCGCAAAC
 IleArgValSerTrpArgProProValLeuThrProThrGlyLeuSerAsnGlyAlaAsn

1930

1950

1970

GTTACCGGCTACGGCGTGTATGCCAAAGGGCAGAGGGTGGCTGAAGTCATCTTCCCCACG
 ValThrGlyTyrGlyValTyrAlaLysGlyGlnArgValAlaGluValIlePheProThr

1990

2010

2030

GCAGACAGCACGGCCGTGGAGCTTGTGCGGCTGCGGAGCCTGGAGGCCAAGGGCGTGACC
 AlaAspSerThrAlaValGluLeuValArgLeuArgSerLeuGluAlaLysGlyValThr

2050

2070

2090

GTGCGGACCCCTCTCGCCCAGGGCGAGTCCGTGGACTCTGCAGTTGCTGCCGTTCCCCCC
 ValArgThrLeuSerAlaGlnGlyGluSerValAspSerAlaValAlaAlaValProPro

2110

2130

2150

GAGCTCCTGGTGCCTCCTACCCCCCACCGAGACCTGCACCCCAATCAAAGCCATTAGCA
 GluLeuLeuValProProThrProHisProArgProAlaProGlnSerLysProLeuAla

2170

2190

2210

AGTTCTGGAGTCCCCGAAACCAAAGACGAGCACCTGGGTCCCCACGCCAGGGATGGATGAG
 SerSerGlyValProGluThrLysAspGluHisLeuGlyProHisAlaArgMetAspGlu

2230

2250

2270

GCCTGGGAGCAGAGCCGTGCACCTGGCCCTGTGCATGGGCACATGCTGGAGGCCCGTG
 AlaTrpGluGlnSerArgAlaProGlyProValHisGlyHisMetLeuGluProProVal

2290

2310

2330

GGCCCCGGAAGGCGGTGCCCTACCCAGCCGCATCCTGCCGCAGCCACAGGGCACCCCCG

GlyProGlyArgArgSerProSerProSerArgIleLeuProGlnProGlnGlyThrPro

2350

2370

2390

GTGTCCACCACCGTCGCCAAGGCCATGGCCGGAGGCCGCGCAGAGGGTGGCGAGAGC
ValSerThrThrValAlaLysAlaMetAlaArgGluAlaAlaGlnArgValAlaGluSer

2410

2430

2450

AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAACGCAGCGCGGGCAGTACGCCGC
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

2470

2490

2510

TCAGACGAGGAGGGACGCCATTGACTCTCCAGACTCAAGAGGAGGGCGCCTCGGTGGAC
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

2530

2550

2570

GACTCCTGAAAGGCTCTGAACCTGGCAAGCAGCCCACTGTTGCCATGGAGACGAGTAC
AspPheLeuLysGlySerGluLeuGlyLysGlnProHisCysCysHisGlyAspGluTyr

2590

2610

2630

CACACAGAGAGCAGCCGGGGTCTGACCTCTCAGACATCATGGAGGAGGACGAGGAGGAG
HisThrGluSerSerArgGlySerAspLeuSerAspIleMetGluGluAspGluGlu

2650

2670

2690

CTGTATTCTGAAATGCAGCTGGAAAGATGGGGAAAGGAGGGGCGCCAGCGCACGTCCCAC
LeuTyrSerGluMetGlnLeuGluAspGlyGlyArgArgArgProSerGlyThrSerHis

2710

2730

2750

AATGCCCTCAAGATTTAGGGAACCCAGCCTCTGCAGGACGGTGGATCACATGGGCCGG
AsnAlaLeuLysIleLeuGlyAsnProAlaSerAlaGlyArgValAspHisMetGlyArg

2770

2790

2810

AGGTTCCCCGTGGCAGCGCTGGCCTCAGAGGTCCCAGCCGTGACAGTCCCATCCATC
ArgPheProArgGlySerAlaGlyProGlnArgSerArgProValThrValProSerIle

2830

2850

2870

GACGATTACGGCGAGACCGCCTTCTCCAGACTCTATGAAGAGTCAGAAACTGACCCT
AspAspTyrGlyArgAspArgLeuSerProAspPheTyrGluGluSerGluThrAspPro

2890 2910 2930
GGTGCCGAAGAGCTCCGGCCGGATCTTGTGGCTCTTTGACTACGACCCGCTCACC
GlyAlaGluGluLeuProAlaArgIlePheValAlaLeuPheAspTyrAspProLeuThr

2950 2970 2990
ATGTCCCCAAACCCAGATGCTGCAGAGGAGGAGCTTCCCTTAAAGAAGGCCAGATCATC
MetSerProAsnProAspAlaAlaGluGluLeuProPheLysGluGlyGlnIleIle

3010 3030 3050
AAGGTTATGGTATAAAGACGCTGATGGATTCTACCGTGGGGAAACCTGTGCCCGGCTT
LysValTyrGlyAspLysAspAlaAspGlyPheTyrArgGlyGluThrCysAlaArgLeu

3070 3090 3110
GGCCTTATTCTTGTAAACATGGCTCTGAGATAACAAGCAGATGATGAGGAGATGATGGAT
GlyLeuIleProCysAsnMetValSerGluIleGlnAlaAspAspGluGluMetMetAsp

3130 3150 3170
CAGCTTCTTAGACAGGGCTTCCTCCCTCTGAATAACACCTGTGGAGAAAATAGAGAGAAC
GlnLeuLeuArgGlnGlyPheLeuProLeuAsnThrProValGluLysIleGluArgSer

3190 3210 3230
AGGAGAAGTGGCAGGCGTCATTGGTATCGACGCCGAGAATGGTGGCCCTGTATGACTAC
ArgArgSerGlyArgArgHisSerValSerThrArgArgMetValAlaLeuTyrAspTyr

3250 3270 3290
GACCCCAGAGAAAGCTGCCAACGTCGATGTCGAGGCCGAACTTACATTTCACAGGA
AspProArgGluSerSerProAsnValAspValGluAlaGluLeuThrPheCysThrGly

3310 3330 3350
GATATTATTACAGTTTGATGAAATTGATGAAGATGGATTATTATGGGGAGCTGAAC
AspIleIleThrValPheGlyGluIleAspGluAspGlyPheTyrTyrGlyGluLeuAsn

3370 3390 3410
GGGCAGAAAGGCCTTGTGCCCTCAAACCTTGGAAAGAAGTGCCTGATGACGTAGAAC
GlyGlnLysGlyLeuValProSerAsnPheLeuGluValProAspAspValGluVal

3430 3450 3470
TATCTTCTGATGCTCCATCCCACTACTCTCAAGATAACGCCAATGCGCTCAAAGGCAAAA

TyrLeuSerAspAlaProSerHisTyrSerGlnAspThrProMetArgSerLysAlaLys

3490

3510

3530

AGGAAGAAGAGTGGTCATTCATACCTAACAGGCAATGTAGCCTCACGTAAGTGAGC
ArgLysLysSerValHisPheIleProEnd

3550

3570

3590

AACTGAAGATAACCGATAAAGATAACCAACTAACGCTAACCTAACCGGGCCAGTGTGGTAGA

3610

3630

3650

CTTAAGGCTTCATTGTGGGGTTAAAAAAAAAAAAGATAAAAGAAATATGTCTCAAAAAA

3670

3690

3710

ACTATTGGACCTAAATAATTAGAATATTACTTGGTCTCAGTTGTAAGCAACTGAATTAA

3730

3750

3770

TAGTGAAGCAAATCATCTTAATAATCATTCTACTATTGCATTAAGAATATTTGAAA

3790

3810

3830

GGCCAACATTGGGAACATATTCTTAACAAGCTAACTGTGTGTTACATAGAGAGAGCTG

3850

3870

3890

CATATTGCATTGTTAGCCACTCTTGGAAAAAGCACAACCTAACAAACATGTTACTATAG

3910

3930

3950

GAAGCTTACTTAGAAACTAACCCAAGGTCAAGCAGATGAGTAGTGAACACAGGTGAT

3970

3990

4010

CGAGTGTGGCTCTGAACACTCCAAACACTGGCTCGAGTGGCCAGAACGTGTTTCCTTA

4030

4050

4070

AGTAACCCTGCCTCTACCTTACGAGAGAGCTATGCTCCTCAAAGCACAATCATCCTG

4090

4110

4130

TGACAGAAGTTGCTGCAACACGCGTTGTTGGTATACCAATGCAACTAAGTTGAT

4150 4170 4190
GAAGCACGCCAGCTCAAATGATCACATTAGATGGAATAGATGGTATCTTCAGGTGTACTTT

4210 4230 4250
GGGATGCTTACTAGGTGTTTCCATTAGAATTAGACCTTGATTTAAATCCAAGCAAGC

4270 4290 4310
TTGAAGCCCCCTGGCTTACAGCATTGCCTGCTGAATACTAAACACTCACATGGCAAGAG

4330 4350 4370
TTGCTCTGGAGAGGTAGGCCAGAGGAATGCTGCTGCACTGCCAACTCAGGCACATGCTT

4390 4410 4430
AGCTGTAAAGGGAAAGCGAGGTGAAGTCGTCCTGCAGCGTATTAGAGTAAAAGTCTACCCC

4450 4470 4490
TCTGAAGCACTATTAAGCGCTAACGTATTTAAATACTACCATGTGCTATCTACTGAG

4510 4530 4550
GAAGATTCAATGTTCAATTATTGGAAATAATGCAAGCATCCACTAAGGCCCTTAAGCTT

4570 4590 4610
TCTTGATTATAATTAAGGTTCAATTAGTTAGTTTTTTTTCTTCACCAGTGTGCCAT

4630 4650 4670
CTCCAATATTCTATAGTATACCAACCACCCAGGAATGCACTTTAACAAATATCAGGATT

4690 4710 4730
TTATATAACCAAATAGTTCAAATACAACAAAATTCCTTATGAACTTCGCTTTAA

4750 4770 4790
GACTACTGATGGGTACTCGGCCAACTTACTATCAACCTAACAGATCATGTCTCCCC

4810 4830 4850
TGCCCTTAGTCTTCATTTATGAAGTGAATTATTACCTGCCTAGCTTGCCAAAGCAACG
4870 4890 4910
GCCACCCCCGCACTCCCTCGAGACAGAGAACGGAACCCACACATTATGTCTGGGCCTC
4930 4950 4970
TCTCTGGCGTGCTGTGGAGAGGACCTTGCTTCTCATGGCATACTCAACAACGTGAAAG
4990 5010 5030
AACAAATGAACCCCCCTGACCTTCCTGGTGGAAACGGGACAGTACGATGTTACCAAG
5050 5070 5090
TGAATTCTGTTGGCGCTCACACACTCAATAAACTGTAACACTGTACCTACTAGGTT
5110 5130 5150
CTCCTGAGGGTTCAGGTACAGCAAGGAGAGCTCCATCCCCACAGTCCATCTCCATTGG
5170 5190 5210
GGTCACCTACGTCATCTATGGTTCTGGTAGTCCTGGAGAGGCAGGGAAATGTCCTCGA
5230 5250 5270
AAAAGAAAAAGGGGCTGCTTCAAAGGCAAGAAACTGCTGAAAAGCTGGTGCAGTGA
5290 5310 5330
AATGATTCATGTGCTTCCGGACAAC TGCCAAATCTATGTAATTTCTTAATTCCAAACT
5350 5370 5390
AGGGCTTCATGACTCAAGTACTTCCTAAAAAAACCAATCTTCTCCCTGACACCAGTA
5410 5430 5450
GAGAAATGCACTTTGCACTACCAACCACTTAAACCAACCACGAGAACAAAGAGGGAGCG
5470 5490 5510

GTTGCTCTGTACCGCTGGCAGTCTGCTCTCATTGTCCAAGCTCTGATTGGGAGGTG

5530 5550 5570
GGAGGGGACGTCTTATTAACAAACGGGGCGCATAGCTATCACCTGTAGCTCCCTCCCTA

5590 5610 5630
CCTGTAATTCCAGTCTTGTGCATTGTCATCTGCCCTAAAGGAATGATTTAACCTT

5650 5670 5690
TCTCCCTCTCAAAATGCTTGCCTCATAATGCATAACTTCACTTGACTCTGGTCTTGA

5710 5730 5750
AATTCCCTAGTTAATTGCCTTGATGTTCTGCCTTATAAAATGCACAATGATTGTACTGT

5770 5790 5810
CTAATAAAAACAGTGTATACTTGTATGTGTCGTGCATTAGTGGCTTCATCCTGACAC

5830 5850 5870
AGTGGTCGAGATCAAGTTGACAGGCTGTGCATTAAAGATACTAGTTCACTTCA

5890 5910 5930
AAGCCAGCCAGGCTACACACAGAAAATGTTACTCAATCATTCAAAAAAGAGAAAAGGAG

5950 5970 5990
AGAAAGTAACTTGTTGGTAAAGCACCAGTACTCCAACCTCCAGAAAGCCGATTATCT

6010 6030 6050
TCATTGCTTTAATGTTCTATTCTGTGGCATATGGTTCTGTTACTTCGTTGTCAAAA

6070 6090 6110
TGCCATACCCAAATACACAGCAATGAATGGCACACAAAGTAATCCACATAATGCATAAGCC

6130 6150 6170
ACACCAAAACCAGACTCAATTAAATCTGCTCCAAATGAGTCCATACCCATCTTCATCAT

6190

6210

6230

TGGCATTGAAACAAAAGACTTACTTACAAAGTTGCTGGCAGATGTATTTGATGGTTACTC

6250

6270

6290

TTTGTAATTCTTGTCCACTTGTAAATTGTTTTACTCTTATAACATACTTTCAGACTG

6310

6330

6350

CCTTCCTTTGTAATTATGGACGGTTATAAATGAATGACAAAGCTTCCCCATTGTGT

6370

6390

6410

CTTCAAAAACGCTATTATAAATTGTAATATAATAGTATGTGGTAGATTATTAAAGG

6430

6450

6470

AAATCCATGTGTGGTTAAGCTCTGTGTGGGTGTGCATGTGCACAGTTAGTGTAAAATA

6490

TTTCTAGAAATAAAATTGTTATTTTAT

FIG. 27K

10 30 50
GGTCCCCACGCCAGGATGGATGAGGCCTGGGAGCAGAACCTGTGCACCTGGCCCTGTGC
MetAspGluAlaTrpGluGlnLysProValHisLeuAlaLeuCys

70 90 110
ATGGGCACATGCTGGAGCCGCCGTGGCCCCGCATCCTGCCACAGCCACAGGGCACCCC
MetGlyThrCysTrpSerArgProTrpAlaProHisProAlaThrAlaThrGlyHisPro

130 150 170
GGTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCGCAGAGGGTGGCGAGAGC
GlyValHisHisArgArgGlnGlyHisGlyProGlyGlyArgAlaGluGlyGlyGluSer

190 210 230
AGCAGGTTAGAGAAAAGGAGCGTCTCCTAGAGAGAACGAGCGCGGGCAGTACGCCGCC
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

250 270 290
TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGGCGCCTCGGTGGAC
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

310 330 350
GACTTCCTGAAAGGCTCTGAACCTGGCAAGCAGGGAAACTGAGGCCACAGAATTGAGAA
AspPheLeuLysGlySerGluLeuGlyLysGlnGlyAsnEnd

370 390 410
TTTTGTCCATGATTACGCAGATGGTCTCTAACAGAGCTGGAATTAGATGAAACCGAGG

430 450 470
CCTGAAGAAGACCTGTTCCACGCCCTTCCCCATGTGCCACGTTCTCCTCACCTATCCAG

490 510 530
GAGTGAATCATCACCTTCCCTGCAATCTGCTCAGGTTACAAACCCGGAGGAAAGGCTGGA

550 570 590
GCACTTGTTCTGGGTGAAGGACCCATACCCCCACTGGTTTGAGATCGGCATTCAGC

FIG. 28A

610 630 650
GCTGTCTTATGGCAGCCMCAGCCCCAGGTGGCCCCAGAGCCCTTGACATGTGGCCACCTG

670 690 710
GGGCTGAGTGTGACTGAGGCCCTGAATTTACTTCTATAAAATTAGTTCCAGATTAGTT

730 750 770
TACATTCTAATTAGTTACATGTAAACAGCCACACGTGGCTGGTGGCCACCAGTGCTGA

790 810 830
CGCCCAGCTCTGGATGACCACACCTGCTACAAGAGATGACTTTCTAGAGAAGAGTAGAA

850 870 890
ACACAGCGGCAGAACACAGCTCTGCACTCCGAGGGCCTCCACTCCTCTGATGAGAC

910 930 950
TGCAGAGGAAGTCTGTTGGCCAAGCATGCTATTAAACACGTTTCCTGCTTGTGTTGTT

970 990 1010
TTAACAGAGCAAACAGGTCTGTTCTATTAAAATTAAAAAGCGTTAATATTCAGC

1030 1050 1070
ATTGTTTATGTTGATTCTAACATAATAACATAATAACATAATTGTTAATATATA

1090 1110 1130
TTGTTAATAATATAATAAACATAAAATAAGTGATACTTATTTCCATTACAGTG

1150 1170 1190
AGATATTCTTAAAAGTAACGTTAAATATTGATTCAATTCAAAGAATACATTCAA

1210 1230 1250
TCATACAGATGGCGTCTGGCTAGGTGACGCATCATGACAGTGGTAGGGAGTGACTGAAGT

1270 1290 1310

TGAGCTGGTGCACAGACTGCCAGTTACAACCCGGGAAGTGTTCCCTGACCATCCGCTT

1330 1350 1370
CCCCATGCTGCCGCCCGTCACATGAGCCCTAACCCCTGGCGCTATCCCATCTGCTCC

1390 1410 1430
AAGACACCGATGTTCTAGTGGGTGGAAGCCTCCACTTTAGTTGACTACGGTATCTCTAG

1450 1470 1490
CATTTCACACATAGTAGGTGCTCAATGAATGTTGTCGAATGAATGAATGAAAGAAGGGA

1510 1530 1550
GGCTGAGAGTAGCTGGACATTGCTCTGAAAAAAATCACCTCCATTCTCCCAATATTACA

1570 1590 1610
AAAGCATTTCATTAAGTCCACAATGAAAAATGCTCACTGTACCAATAATAATATCTT

1630 1650
AGTTATCTATTTAAAAGTAAAAAAAAACCTCGTGCCGAAGTC

FIG. 28C